

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 18:03:15 ; Search time 19 Seconds
(without alignments)
1551.496 Million cell updates/sec

Title: US-09-715-927-6
Perfect score: 2929
Sequence: 1 MTRAGDHNRRQCGCGSLADY.....ACGPDKEVRKENQNTSVV 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/FACTUS-COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1799	61.1	383	4	US-09-149-476-460 Sequence 460, Ap
2	1336	4.6	591	4	US-09-540-236-2490 Sequence 2490, Ap
3	123.5	4.2	524	2	US-08-928-692-12 Sequence 12, Appl
4	123.5	4.2	524	4	US-09-339-972-12 Sequence 12, Appl
5	117	4.0	490	4	US-09-489-039A-13226 Sequence 13226, A
6	113.5	3.9	329	4	US-09-489-039A-14206 Sequence 14206, A
7	112	3.8	305	4	US-09-252-991A-33032 Sequence 33032, A
8	110	3.8	429	4	US-09-328-352-4392 Sequence 4392, Ap
9	109.5	3.7	470	4	US-09-134-001C-4610 Sequence 4610, Ap
10	108	3.7	330	5	US-08-118-270-19 Sequence 19, Appl
11	108	3.7	330	5	US-09-134-001C-4610 Sequence 19, Appl
12	108	3.7	549	4	US-09-489-039A-8237 Sequence 8237, Ap
13	108	3.7	618	4	US-08-595-553A-2 Sequence 2, Appl
14	108	3.7	618	4	US-09-540-1960-4 Sequence 4, Appl
15	107.5	3.7	491	4	US-09-543-681A-8251 Sequence 8251, Ap
16	107.5	3.7	897	4	US-09-543-681A-4249 Sequence 4249, Ap
17	107	3.7	411	4	US-09-134-001C-3299 Sequence 3299, Ap
18	107	3.7	465	4	US-09-328-352-5222 Sequence 5222, Ap
19	107	3.7	512	4	US-09-540-236-3548 Sequence 3548, Ap
20	104	3.6	534	2	US-09-031-392-4 Sequence 4, Appl
21	104	3.6	534	3	US-09-299-543-4 Sequence 4, Appl
22	104	3.6	534	4	US-09-610-417-4 Sequence 4, Appl
23	103.5	3.5	471	4	US-09-328-314-17 Sequence 17, Appl
24	103	3.5	358	2	US-08-748-485-6 Sequence 6, Appl
25	103	3.5	718	4	US-09-657-960-3 Sequence 3, Appl
26	102.5	3.5	443	4	US-09-489-039A-8166 Sequence 8166, Ap
27	102.5	3.5	529	4	US-09-291-922-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-149-476-460
; Sequence 460, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23

28 102 3.5 553 4 US-09-134-001C-2974 Sequence 2974, Ap
29 101.5 3.5 996 4 US-09-252-991A-27018 Sequence 27018, A
30 100.5 3.4 411 3 US-09-236-080-6 Sequence 6, Appl
31 100.5 3.4 760 4 US-09-252-991A-27790 Sequence 27790, A
32 100 3.4 319 4 US-09-543-681A-5398 Sequence 5398, Ap
33 100 3.4 499 4 US-09-134-001C-5370 Sequence 5370, Ap
34 100 3.4 510 4 US-09-489-039A-9866 Sequence 9866, Ap
35 99.5 3.4 461 1 US-08-194-338-4 Sequence 4, Appl
36 98.5 3.4 411 3 US-09-236-080-2 Sequence 2, Appl
37 98.5 3.4 411 3 US-09-336-643A-83 Sequence 83, Appl
38 98 3.3 366 4 US-09-134-001C-5502 Sequence 5502, Ap
39 98 3.3 443 4 US-09-134-001C-3227 Sequence 3227, Ap
40 98 3.3 772 4 US-09-134-000C-6491 Sequence 6491, Ap
41 98 3.3 808 4 US-09-134-001C-3105 Sequence 3105, Ap
42 97.5 3.3 596 4 US-09-252-991A-48031 Sequence 26031, A
43 97.5 3.3 808 2 US-08-629-291A-33 Sequence 33, Appl
44 97.5 3.3 808 2 US-08-658-335B-33 Sequence 33, Appl
45 97.5 3.3 808 4 US-09-406-640-33 Sequence 33, Appl

1	EARLIER FILING DATE: 1997-08-22
2	EARLIER APPLICATION NUMBER: 60/056,894
3	EARLIER FILING DATE: 1997-08-22
4	EARLIER APPLICATION NUMBER: 60/056,911
5	EARLIER FILING DATE: 1997-08-22
6	EARLIER APPLICATION NUMBER: 60/056,636
7	EARLIER FILING DATE: 1997-08-22
8	EARLIER APPLICATION NUMBER: 60/056,874
9	EARLIER FILING DATE: 1997-08-22
10	EARLIER APPLICATION NUMBER: 60/056,910
11	EARLIER FILING DATE: 1997-08-22
12	EARLIER APPLICATION NUMBER: 60/056,864
13	EARLIER FILING DATE: 1997-08-22
14	EARLIER APPLICATION NUMBER: 60/056,631
15	EARLIER FILING DATE: 1997-08-22
16	EARLIER APPLICATION NUMBER: 60/056,845
17	EARLIER FILING DATE: 1997-08-22
18	EARLIER APPLICATION NUMBER: 60/056,892
19	EARLIER FILING DATE: 1997-08-22
20	EARLIER APPLICATION NUMBER: 60/057,761
21	EARLIER FILING DATE: 1997-08-22
22	EARLIER APPLICATION NUMBER: 60/047,595
23	EARLIER FILING DATE: 1997-05-23
24	EARLIER APPLICATION NUMBER: 60/047,599
25	EARLIER FILING DATE: 1997-05-23
26	EARLIER APPLICATION NUMBER: 60/047,588
27	EARLIER FILING DATE: 1997-05-23
28	EARLIER APPLICATION NUMBER: 60/047,585
29	EARLIER FILING DATE: 1997-05-23
30	EARLIER APPLICATION NUMBER: 60/047,586
31	EARLIER FILING DATE: 1997-05-23
32	EARLIER APPLICATION NUMBER: 60/047,590
33	EARLIER FILING DATE: 1997-05-23
34	EARLIER APPLICATION NUMBER: 60/047,594
35	EARLIER FILING DATE: 1997-05-23
36	EARLIER APPLICATION NUMBER: 60/047,589
37	EARLIER FILING DATE: 1997-05-23
38	EARLIER APPLICATION NUMBER: 60/047,593
39	EARLIER FILING DATE: 1997-05-23
40	EARLIER APPLICATION NUMBER: 60/047,614
41	EARLIER FILING DATE: 1997-05-23
42	EARLIER APPLICATION NUMBER: 60/043,578
43	EARLIER FILING DATE: 1997-04-11
44	EARLIER APPLICATION NUMBER: 60/043,576
45	EARLIER FILING DATE: 1997-04-11
46	EARLIER APPLICATION NUMBER: 60/047,501
47	EARLIER FILING DATE: 1997-05-23
48	EARLIER APPLICATION NUMBER: 60/043,670
49	EARLIER FILING DATE: 1997-04-11
50	EARLIER APPLICATION NUMBER: 60/056,632
51	EARLIER FILING DATE: 1997-08-22
52	EARLIER APPLICATION NUMBER: 60/056,664
53	EARLIER FILING DATE: 1997-08-22
54	EARLIER APPLICATION NUMBER: 60/056,876
55	EARLIER FILING DATE: 1997-08-22
56	EARLIER APPLICATION NUMBER: 60/056,881
57	EARLIER FILING DATE: 1997-08-22
58	EARLIER APPLICATION NUMBER: 60/056,909
59	EARLIER FILING DATE: 1997-08-22
60	EARLIER APPLICATION NUMBER: 60/056,875
61	EARLIER FILING DATE: 1997-08-22
62	EARLIER APPLICATION NUMBER: 60/056,862
63	EARLIER FILING DATE: 1997-08-22
64	EARLIER APPLICATION NUMBER: 60/056,887
65	EARLIER FILING DATE: 1997-08-22
66	EARLIER APPLICATION NUMBER: 60/056,908
67	EARLIER FILING DATE: 1997-08-22
68	EARLIER APPLICATION NUMBER: 60/048,964
69	EARLIER FILING DATE: 1997-06-06
70	EARLIER APPLICATION NUMBER: 60/057,650
71	EARLIER FILING DATE: 1997-09-05
72	EARLIER APPLICATION NUMBER: 60/056,884
73	EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Best Local Similarity 92.4%; Pred. No. 9.9e-175;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 NAVGQIMTFGSPVIGCGFISGNLVSMCVYVLLWKVYQKTPALAVKAGLKEEBTELKOL 249
DB 1 NAVGQIMTFGSPVIGCGFISGNLVSMCVYVLLWKVYQKTPALAVKAGLKEEBTELKOL 60
QY 250 NLHKTEPKLEGTHLMGVKDSNIHELEHEQPTCASQMAEPFRTRFDGWVSYNQPVFL 309
DB 61 NLHKTEPKLEGTHLMGVKDSNIHELEHEQPTCASQMAEPFRTRFDGWVSYNQPVFL 120
QY 310 AGMGLAFYMTVLGPDCTTGYAYTQGLSGSILSMGASAITGIMGTVAFTWLRKCGL 369
DB 121 AGMGLAFYMTVLGPDCTTGYAYTQGLSGFHPQVFDGSIYNNWNGNCSFYLATSKWVF 180
QY 370 VETGLISGLAQLSCILCVISVFMFGSPDLDSVSPFFEDIRSRFQGESITPTKIPETITE 429
DB 181 GSAGLISGLAQLSCILCVISVFMFGSPDLDSVSPFFEDIRSRFQGESITPTKIPETITE 240
QY 430 IYMSNGSNSANIVPETSPEVPIISVLSLLFAGVIAARIGLWSFDLTVTLQLOENVISER 489
DB 241 IYMSNGSNSANIVPETSPEVPIISVLSLLFAGVIAARIGLWSFDLTVTLQLOENVISER 300
QY 490 GIINGVQNSMNYLLDLHFIHIVILAPNPEAGLLVLISVSFVAMGHIMYFPAQNTLGNK 549
DB 301 GIINGVQNSMNYLLDLHFIHIVILAPNPEAGLLVLISVSFVAMGHIMYFPAQNTLGNK 360
QY 550 LFCAGPDAKEVKENQANTSVV 571
DB 361 LFCAGPDAKEVKENQANTSVV 382

RESULT 2
US-09-540-236-2490
; Sequence 2490, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2490
; LENGTH: 591
; TYPE: PRT
; ORGANISM: M.cattarhalis
US-09-540-236-2490

Query Match      4.6%; Score 136; DB 4; Length 591;
Best Local Similarity 19.2%; Pred. No. 6.3e-05;
Matches 120; Conservative 94; Mismatches 228; Indels 182; Gaps 27;

QY 18 ADVLTSAXELLVGHSLTSWGDMMHFAVSVELV----- 51
DB 52 ADMVSAASISWAG-MLANGG-----YASAYLMGTGCVLLALLAPYLKFKGFTVP 105
QY 52 -----ELYNSLLTAVYGLVAGSVLVGLGAIIGDWDKNARKV-AQTSLVVQNVSVIL 105
DB 106 DFIDGRFYKTAFLVAVVCLILACTTYVIGQMTGAGVAFSREFLYDSNTGLIIAIVLVF 165
QY 106 CGILLMM-----VFLHKHLLTVMHGVLTSCYILITIAN-----IANLASTATAITQ 155
DB 166 YAVLGNKKITTVQVQAQVCLVAVYIIPAFISLNTGNPIQMGFGNDVSTGMPILOK 225

156 RDWIVVWAGEDRSKLANMNATIRIDQLTNILAPMAVGQIMTFGSPVIGCGFI----- 208
226 LDMVLADLG-----FAQYTADVP--NKLNMFLTWSL-MIGTAGLPHVIRFTVPKVS 277
209 -----SCWNLVSMCVYVLLWKVYQKTPALAVKAGLKEEBET-----ELKQLNLHKDTEP--- 257
278 ARISAGWTLIFIAL-----LYTTAPAVGSMARLNINIVYPOGLNQPALAYEARPEWM 330
258 KPLEGTHLMGVKDSNIHELEHEQPTCASQMAEPFRTRFDGWVSYNQPVFLAGMGLAFL 317
331 KWWTETGLLKYEDKN-----NDGLIQYNDK----- 356
318 YMTVLGDFDCTTGYAYT-----OGLSGSILS-----ILMGASAITGIMGTVAFTWLRKCG 368
357 -----NBEYATVTAEBGWQGNELTANNDILVLANPEIANLP-----SWV---IG 398
369 LVRTGLISGLAQLSCILCVISVFMFGSPDLDSVSPFFEDIRSRFQGESITPTKIPETITE 428
399 LIAAGGLAALSTAAGLLLAISAISHDLIKTKIP--DINDK---GELMAARISMTIAI 453
429 EYMSNGSNSANIVPETSPEVPIISVLS--LFAGVIAARIGLWSFDLTVTLQLOENVI 485
454 VVATYLMGNPPGPTAQWAVAFGIAASSLFPALMMGIFSKRI-----NST 498
486 ESERGIINGVQNSMNYLLDLHFIHIVILAP-----NPEAFGLLVLSVSFVAMGHIMYF 539
499 GATAGMIAGLSATCIIVFLYMGWFFI---PGTNSFKVNEANWILGVSPUSFGAIGAVINP 555
540 --RFAQNTLGNKLFACGPDACEVR 561
556 IVAIAVSAMGN-----PPPKEVQ 573

RESULT 3
US-08-928-692-12
; Sequence 12, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Iaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 524 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
; US-08-928-692-12

Query Match      4.2%; Score 123.5; DB 2; Length 524;
Best Local Similarity 20.3%; Pred. No. 0.001;
Matches 99; Conservative 69; Mismatches 150; Indels 169; Gaps 23;

QY 41 MHFAVSVELV-----ELVNSL--LLTAVYGLVAGSVLVGLGAIIGDWDVKNARLKVAQ 93
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 94 TSLAV---QNVSVILGIIIMVFLHKLHLLTHYHGWLTSCYIIIIITIANIANLASTAT 150
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 150 SHIIITAGSISGLYCGLI-----SGLVPMY-----IGEIAPTA- 183
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 151 AITIQRDWIVVAGEDRSKLANNNATIRIDOLTNILAPMAVGQIMTFGSPVIGCGFISG 210
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 -----LRGALGTFHQLAIVTGILI-----SQIIGLEFILG 213
QY 211 -----WNL-----VSMCVYVLLKVKYQKTPALAVKAGLKEBETELKQNLHKTPEKPL 260
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 214 NYDLWHILGLSGVRAILQSLLLFFCPSPRYLYIKL---DEEVAKQ-SLKR----- 262
QY 261 EGTMLMGVKD--SNHLEHEOEPTCASOMAEPPFTFRDGMVSYYNQPVFLAGM-GLAFL 317
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 ----LRGYDDVTKDINEMKEREESSEQKYSIIQLFTN---SSYRQPIVVALMLHVAQ 315
QY 318 YMTVLGDCITTYAYTQGLSGSIILMGASAITGIMGTVAFTWLRKCGLVRTGLISG 377
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 316 FSGINGIFYYSTISIFQTAGISKPVYATI-GUGAVNMVF-TAVSVFLVEKAGRRSLFLIGM 373
QY 378 LAQLSCLI-----LCVISVMPGSPDLVSPPEDIRSRFIQGESITP 420
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 374 SGMFVCAIFMSVGLVLLNKFMSVSMIAIF-----LFVSFFE-----IGP 415
QY 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIIS-----VSLL 458
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 469 FAGVLLA 475
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RESULT 4
US-09-339-972-12
; Sequence 12, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; PRIOR APPLICATION NUMBER: US 60/117,747
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 524 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6323002e
; US-09-339-972-12

Query Match      4.2%; Score 123.5; DB 4; Length 524;
Best Local Similarity 20.3%; Pred. No. 0.001;
Matches 99; Conservative 69; Mismatches 150; Indels 169; Gaps 23;

QY 41 MHFAVSVELV-----ELVNSL--LLTAVYGLVAGSVLVGLGAIIGDWDVKNARLKVAQ 93
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 94 TSLAV---QNVSVILGIIIMVFLHKLHLLTHYHGWLTSCYIIIIITIANIANLASTAT 150
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 150 SHIIITAGSISGLYCGLI-----SGLVPMY-----IGEIAPTA- 183
QY 151 AITIQRDWIVVAGEDRSKLANNNATIRIDOLTNILAPMAVGQIMTFGSPVIGCGFISG 210
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 -----LRGALGTFHQLAIVTGILI-----SQIIGLEFILG 213
QY 211 -----WNL-----VSMCVYVLLKVKYQKTPALAVKAGLKEBETELKQNLHKTPEKPL 260
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 214 NYDLWHILGLSGVRAILQSLLLFFCPSPRYLYIKL---DEEVAKQ-SLKR----- 262
QY 261 EGTMLMGVKD--SNHLEHEOEPTCASOMAEPPFTFRDGMVSYYNQPVFLAGM-GLAFL 317
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 ----LRGYDDVTKDINEMKEREESSEQKYSIIQLFTN---SSYRQPIVVALMLHVAQ 315
QY 318 YMTVLGDCITTYAYTQGLSGSIILMGASAITGIMGTVAFTWLRKCGLVRTGLISG 377
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 316 FSGINGIFYYSTISIFQTAGISKPVYATI-GUGAVNMVF-TAVSVFLVEKAGRRSLFLIGM 373
QY 378 LAQLSCLI-----LCVISVMPGSPDLVSPPEDIRSRFIQGESITP 420
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 374 SGMFVCAIFMSVGLVLLNKFMSVSMIAIF-----LFVSFFE-----IGP 415
QY 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIIS-----VSLL 458
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 459 FAGVIAA 465
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 469 FAGVLLA 475
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-489-039A-13226
; Sequence 13226, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
```

; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13226
 ; LENGTH: 490
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13226

Query Match 4.0%; Score 117; DB 4; Length 490;
 Best Local Similarity 18.5%; Pred. No. 0.0042;
 Matches 95; Conservative 62; Mismatches 138; Indels 218; Gaps 25;

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QY 3 RAGDNRQGGCGSLADYLTSAKELLYLGHLSLSTWGBMHFAVSVELVELY-----54
DB 9 RADEN-----CCDSL-----ISIEGTTMQ--AILSFTEIFSQPAFLMG 47

QY 55 -----GNSLL-----LTAVVGLVVA-----GSVLVGLAIGDWD 84
DB 48 LIAFVGLVALRSPGNKLLTGTLKPILGYLMSAGAGVIVANLPLGGIIEAGNIRVIP 107

QY 85 KN-ARKVQAQTSLVQNVSVILCGHILMMVFL-----HGHELLTMYHGWLTSCVILITI 139
DB 108 NNEAIVSAQKMLGVETMSILLGLFIFNLIIARCTKYKIFLTGHHGFFLACLESAYLQA 167

QY 140 ANIANLASTATAITIQRDWIVVAGEDRSKLANNNATIRIDQTNILAPMAVQIMTFG 199
DB 168 AEF-----QWMLLIG-----179

QY 200 SPVIGCGFISG-WNLVSMCVEXVLLMKVYKTPALAVKAGLKBEBTELKQNLNKHDTPEK 258
DB 180 -----GFLGWSAIS-----PAIG-----QRYTRQVTE-- 203

QY 259 PLEGTHLMGVKDSNIHELEHQEPTCASQMAEPFTRPDGWS-----YINQPVLAGMGL 314
DB 204 --DG-----GIANGHFGSGJYVLSAWIARSTGNPANSFADTSEISKWGLRDTTVTG-- 254

QY 315 APLVMTVLGFDG-ITGYAYTQGLSGS-----ILSILMGASAITGIMGTVAFTWLRKCGLV 370
DB 255 --IVMFVIYFVCSAVAGSAYLSTIDQNLIFSVLTG-QFAVG--AIVYNGVR-----304

QY 371 RTGLISGLAQLSCILCVISVMPGSPDLVSPPEDIRSRFIOGESITPKIEITTEI 430
DB 305 ---LILG-----DL-VPAFGISQKLI-----PDSIPAVDCAV 333

QY 431 YMSGNSGANIVETSPRSVPITISVLLPAGVI 463
DB 334 FFT-----FSPITAVVGVFISFVGGVLV 355
  
```

RESULT 6
 US-09-489-039A-14206
 ; Sequence 14206, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 14206
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-14206

Query Match 3.9%; Score 113.5; DB 4; Length 329;
 Best Local Similarity 20.1%; Pred. No. 0.005;
 Matches 78; Conservative 55; Mismatches 133; Indels 123; Gaps 15;

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QY 45 AVSVFLVELYGNLSLLLTAVYGLVWAGSVLVGLAIGDWDVKNARKLVKACTSLVQNVSVI 104
DB 25 AMTAFELQQLINGLTGLGAVYGLAIGYTMVYG-IIG-----MINFAHGE--VTWVSAY 74

QY 105 LC--GIILMMVF-LHKHELL-----TWYHGWLTSCVILITIITIANLASTAT 150
DB 75 LCAIGALLSFFGIHSPFLLIFATLVFTVTVGVGWAIER--IAYRPLENSTRAPLIS 132

QY 151 AI---TIQRDWIVVAGEDRSKLANNNATIRIDQTNILAPMAVQIMTFGSPVIGCOF 207
DB 133 AIGMSLILQNVYQLSQPNQOQIPTLLSGALR-----MTVGDGVYQITW 176

QY 208 ISGNLVSMCVEXVLLMKVYKTPALAVKAGLKBEBTELKQNLNKHDTPEKPLEGTHLMG 267
DB 177 TKVFIILVAALVGLMLTIIQYTRIGRICRATQQR-----RVAAILG 219

QY 268 VKDSNIHELEHQEPTCASQMAEPFTRPDGWSYINQPVFLAGMGLAFLYMTVLGFDGI 327
DB 220 INTDRVISL-----VFVIGAAAGLAGVL-----V 244

QY 328 TTGYAYTQGLSGSILSILMGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQ-----380
DB 245 TMNYGTDFYIGIIGIKAFATAVLGGIGSLP-----GAMUGLGLLVGAEOAFAGLV 296

QY 381 -----LSCLILCVISVEMP-----GSPL 398
DB 297 NSDYKDVFSFALLVAILIFRPQGLLGRPL 325

RESULT 7
US-09-252-991A-33032
; Sequence 33032, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33032
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33032
  
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```

Query Match 3.8%; Score 112; DB 4; Length 305;
Best Local Similarity 18.3%; Pred. No. 0.0063;
Matches 71; Conservative 65; Mismatches 112; Indels 140; Gaps 16;

QY 48 VFLVELYGNLSLLLTAVYGLVWAGSVLVGLAI-----IGDWVKNARKLVKACTSLV----97
DB 5 IFLQOMI-NGLTGSYVGLAIGYTMVYGIHGINFAHGEVYIMSAIALLAFAFG 63

QY 98 VQNVSVILCGIILMMVFLHKHELLTMYHGWLTSCVILITIITIANLASTATAI---TI 154
DB 64 LQNFPLLILGTLFTV-----LVTCYGMVIER--IAYKPLENSTRAPLISAIKMSLI 115

QY 155 QRDWIVVAGEDRSKLANNNATIRIDQTNILAPMAVQIMTFGSPVIGCOFIS-----209
DB 116 LQNVVQAQGPQQGI-----PTLDDGALKFH---VGDGFEVQLTYTK 154

QY 210 -----GWNLVSMCVEXVLLMKVYKTPALAVKAGLKBEBTELKQNLNKHDTPEKPL 260
DB 155 LFIILASLIGNAVITVYIRYTKLGRCRAT-----QQDRKM-----190

QY 261 EGTLMGVKDSNIHELEHQEPTCASQMAEPFTRPDGWSYINQPVFLAGMGLAFLYMT 320
  
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Db 191 --ASILGINTDRV-----ISY-----VFVIGAAVAGV 218
QY 321 VLGFDCITTYGAVTQGLSGSILMSGASITGIMGTVAFTWLRKCGLVRTGLISGLAQ 380
Db 219 L-----ITWNYGTFYAGFIGIGIKAFANVLGGISLP-----GAMLGGLVLGVAE 265
QY 381 -----JSCLLICVSWPMP 394
Db 266 AQFSGMVTYDKDVFASFLLVILIFRP 293

RESULT 8
US-09-328-352-4392
; Sequence 4392, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4392
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4392

Query Match 3.8%; Score 110; DB 4; Length 429;
Best Local Similarity 19.8%; Pred. No. 0.018;
Matches 91; Conservative 78; Mismatches 158; Indels 132; Gaps 23;

QY 20 YLTSAKELLY--LGHS---LSTGDRMHFAVSVFLVLYGNSLLLT----- 62
Db 4 YDIIRIYFNDLSHSYFLLTMTTSTHQSQSLIYM-LIGSAILALSLGVRHGFGLYL 62
QY 63 -----VYGLVAGSVVLGAI---IGDWDRKVARLKVAQTSLLVQNVSVILCG 107
Db 63 VPMSEHFGQGHVFSLATAMQNLINGAIOPTGATADKYG-----SKVVVTVGGLLYT 115
QY 108 I-ILMVFLHKLHLLTMVHGWLTCYLIITIANIANLASTAITTORDMIVVWAGED 166
Db 116 LGLLLMF-----SSSVLIILNLSGLIIGALSATSFTVLLSAVGRAAPPE 161
QY 167 RSKLANMATIRRIDQTLNLAAPVAGIOMTFGSPVCGGHSWN-----LVSMCV 218
Db 162 KRSMAAGIAS-----AAGSGQFIMLPSTLLLLKTV-GWSSALMVSAALLIALII 209
QY 219 EYVLLKVVYQKTPALAVKAGLKEETELKQLNLHKDTEPKP-----LEG 262
Db 210 P-LAWML--KGPSNOTPKAIAQPOLTPKQV-LHIAKHKPFWWALGFLVCGFQVVFLG 264
QY 263 THLMGVKDSNIHELHEHEOPTCAS-----QMAEPPRTFRGWV-SYVNPVFLAGM--- 312
Db 265 VHLPG-----YLIHGHFDATTGTFLALVLFNIVGTGAGWLGDRFSKPKLLMALYGS 318
QY 313 -GLAFLYMTVLGFDCTTGYAY-----TQGLSGSILMSGASAITGIMGTVAFT 361
Db 319 RGIAIIAFLLLPLSTYTV-YAFGIIMGLMLWLTSTVPLTNGIVANFEGVKYLSMLSGIVFFT 377
QY 362 WLRKCGLVRTGLISGL-----AQUSCLILCVISVFMFG 395
Db 378 ---HQVGSFFGWLGVGNHDLTGNYNALWLCISALSILG 413

RESULT 9
US-09-134-001C-4610
; Sequence 4610, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4610
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4610

Query Match 3.7%; Score 109.5; DB 4; Length 470;
Best Local Similarity 19.5%; Pred. No. 0.023;
Matches 100; Conservative 85; Mismatches 190; Indels 137; Gaps 21;

QY 73 LVLGAIIGDWD-----KNARKKVAQTSLVQNVSVILCGIILMMVFL 115
Db 45 LILGTIFLDAYDITILGTWTDQTLQOQHLSPATLSIVMTSLFIFGALFGALGGTLAYQFG 104
QY 116 HKHELLTMVHGWLTCYLIITIANI-ANLASTATITIQORDWIVWVAGEDR----- 167
Db 105 RKR-----ILSIALLTITVTSLGAAALAPNVILLICRCINGFAGMDSPVAFTFI 154
QY 168 SKLANMATIRRID--QLTNILAPVAGIOMTFGSPVCGG-----FISGMNLVSMCVVEY 220
Db 155 AEISNLKHKGRNVNVQVWVYVAIVTSALAVT-AFFMLGAGAHLRVAVGFGALIAFVLY 213
QY 221 VLLKVVYQKTPALAVKAGLKEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQ 280
Db 214 ILIRKVLHSPSTVWINHVSLEXATEFIRKYHKD-----IHLEGLEDDLN----- 259
QY 281 EPTCASQMAEPRTFRDGMVSYNQPFLA-----GMGLAFLYMTVLGFDCT 328
Db 260 ----SDVTSPHNSWTDLPKPYIKRIILATAISTLQGMQYVGVG---LYPIIA----- 306
QY 329 TGVAYTQGLSGSILMSGAS--ITGIMGTVAFTWLRKCGLVRTGLISGLAQSLIL 386
Db 307 ----TYLISKDKIGVLLGTAVINAGILGAYLGAQLTYKLGTRKLTMI-GFTLVLLSMV 360
QY 387 CVISVFMGSPDLDSVSPEDIRSFIOGESITP-TKIPEITTEIYMGNSGNSANIVPET 445
Db 361 CV-GLFYHLPMLNTF---LIGLFLGHSGGPGTGKTCIGALSFPTHLRSQATGFVES 415
QY 446 SPESVPIISVSLFPAGVIAARIGLMSFDLTVTOLLQENVIESERGIINGVQNSMYLLDL 505
Db 416 VERTGSIIGTFVF--PIILAAVGLTN----- 439
QY 506 LHPFIVILAPNPEAFGLLVLSVSVFVANG-HI 536
Db 440 ---TWLLLSIVP-LIGIITVSIKWEAVGKHI 467

RESULT 10
US-08-118-270-19
; Sequence 19, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

```
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/118,270
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 330 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-118-270-19

Query Match 3.7%; Score 108; DB 1; Length 330;
Best Local Similarity 24.4%; Pred. No. 0.019;
Matches 51; Conservative 39; Mismatches 71; Indels 48; Gaps 11;

QY 60 LTAIVGLV----VAGSVLVGLAIGDWDKNARKVAQTSLVQNVSVILCGIILMMVFL 115
Db 4 LAAVGFLIVFTVGVNVLVIAVL-----TSRALRAPQNLFLVSIASADILVATLVMPFS 58

QY 116 HKHELLTMHGVLTSCYILITI---ANIANLASTATAITIQRDWIVVVGEDRSKLAN 172
Db 59 LANEIMWYFGQWCGVLAIDVLFCTSSIVHLC-----AISLDYKSWTQAVE-----YN 109

QY 173 MNATIRRIDLTNILAPMAVGQIMTF-----GSPVTCGF-IGSNLVSMCVE- 219
Db 110 LKRTPRVK--ATIVAVWLISAVISFPPLVSLYRQPDGAAYPQCGLNDETWTYILSSCIGS 167

QY 220 -----YVLW-KVY-----OKTPALAVK 236
Db 168 FPAPCLIVLLVARIYAKRTRTISEK 196

RESULT 11
PCT-US93-08528-19
/ Sequence 19, Application PC/TUS9308528
/ GENERAL INFORMATION:
/ APPLICANT: New York University
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM: disk
/ MEDIUM TYPE: Floppy
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08528
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
```

```
/
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 330 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US93-08528-19

Query Match 3.7%; Score 108; DB 5; Length 330;
Best Local Similarity 24.4%; Pred. No. 0.019;
Matches 51; Conservative 39; Mismatches 71; Indels 48; Gaps 11;

QY 60 LTAIVGLV----VAGSVLVGLAIGDWDKNARKVAQTSLVQNVSVILCGIILMMVFL 115
Db 4 LAAVGFLIVFTVGVNVLVIAVL-----TSRALRAPQNLFLVSIASADILVATLVMPFS 58

QY 116 HKHELLTMHGVLTSCYILITI---ANIANLASTATAITIQRDWIVVVGEDRSKLAN 172
Db 59 LANEIMWYFGQWCGVLAIDVLFCTSSIVHLC-----AISLDYKSWTQAVE-----YN 109

QY 173 MNATIRRIDLTNILAPMAVGQIMTF-----GSPVTCGF-IGSNLVSMCVE- 219
Db 110 LKRTPRVK--ATIVAVWLISAVISFPPLVSLYRQPDGAAYPQCGLNDETWTYILSSCIGS 167

QY 220 -----YVLW-KVY-----OKTPALAVK 236
Db 168 FPAPCLIVLLVARIYAKRTRTISEK 196

RESULT 12
US-09-489-039A-8237
/ Sequence 8237, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27
/ PRIOR APPLICATION NUMBER: US 60/117,747
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 14342
/ SEQ ID NO 8237
/ LENGTH: 549
/ TYPE: PRT
/ ORGANISM: Klebsiella pneumoniae
/ US-09-489-039A-8237

Query Match 3.7%; Score 108; DB 4; Length 549;
Best Local Similarity 20.5%; Pred. No. 0.042;
Matches 76; Conservative 51; Mismatches 134; Indels 110; Gaps 13;

QY 37 WGDMMHFAVSVFLVELYGNLSLLTAVYGLVAVAGSVLVGLAIGDWDKNARKVA-QTS 95
Db 10 WRQYRWFPLGVIAL-----SLSAALGIGLIAFI-----NLRUITAVDTS 49

QY 96 LVQNVSVILCGIILMMVFLHKHELLTMHGVW--LTSCVILITITIANLASTATAIT 153
Db 50 LRVLPFELGLLGLLMAVTLGSQLATLTGLHHFVYLRGRGEVKRILDTQIEQEKIGSA-- 107

QY 154 IQRDWIVVVGEDRSKLANNATIRRIDLTNILAPMAVGQIMTFGSPVTCGFISG--- 210
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Db 108 -----SLLAGLTSIDIRITIAFVRLPELVQGLIFGSAAY-LAWLSGKMM 152
Qy 211 -----WNLVSMCVYVLLMKVYQKTPALAVKAGLKEETEL-----KQNLHKO 254
Db 153 LVTALMALTWGGFVLVSRVYKH-----MASLRETEKLYHDYQTVLEGRKELTLNRE 206
Qy 255 TEPKPLEGTHLMGVKDSNIHELEHEQEPFCASQMAEPERTFRDGVSYNQPVFLAGWGL 314
Db 207 RBYVFNQYLDPAREYRHIVR-----ADTFHLSAVNW-----SNIMMLGAILG 251
Qy 315 AFLYMTVLGFCITTCYAYVTOGLSGSILMSAGSAITGIMGTVAFTWLRKRCGLVRTGL 374
Db 252 VFWMANSLGW-----ADTAAVATYSLTL-----FLRPTL 281
Qy 375 ISGLAQLSCLI 385
Db 282 LSAVGALPTLL 292

RESULT 13

US-08-595-553A-2

; Sequence 2, Application US/08595553A
; Patent No. 6391579
; GENERAL INFORMATION:
; APPLICANT: NANCY CARRASCO, ET AL.
; TITLE OF INVENTION: THYROID SODIUM/IODIDE SYMPORTER AND
; TITLE OF INVENTION: NUCLEIC ACID ENCODING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,553A
FILING DATE: FEBRUARY 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG J. ARNOLD
REGISTRATION NUMBER: 34,287
REFERENCE/DOCKET NUMBER: 96700/393
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: YES
ORIGINAL SOURCE:
INDIVIDUAL: RAT
ORGANISM: RAT
INDIVIDUAL ISOLATE: SODIUM/IODIDE SYMPORTER

US-08-595-553A-2

Query Match 3.7%; Score 108; DB 4; Length 618;

Best Local Similarity 19.1%; Pred. No. 0.051;

Matches 103; Conservative 71; Mismatches 160; Indels 204; Gaps 27;

Qy 14 CGSLADYLTSAKFLLYGLHSLTWGDRMWHFAVSFLVELYGNLSLLLTAVYGLVAGSVL 73
Db 132 CGTL-QYLVAT--MLYTG-----IIVAPALILNQVTGLDIWASLL 169

Qy 74 VLGAIGDWVKNARLKVAQTSIVVQNVSVILCGIILMMVFLHKHELLTMYHGWL-LTSC 132
Db 170 STGIITLTLYTGGMKAVVWTD--VFQVVVMLVGF-----WILARG 209
Qy 133 YILIIITIANIANLATAITTIQ-----RDWIVVVG-----164
Db 210 VILGGPRNVLSLAQNHRSINLMDPDPDRSRYTFTWTFVGGTLVWLSMGVYQVQAQVRY 269
Qy 165 -----EDRSKLANMNATIRIDQLTNILAPMAVGQIMTFGSPVIGCGFTSGNLSVMCWE 219
Db 270 VACHTEGKAKLALL-----VNQL-----GLFLIVASAC-CG-----300
Qy 220 YVLLMWVYQK--TPALAVKAGLKEETELKQNLHAKDTEPKP-----LEGTH 264
Db 301 --IVMFVYKDCDPLLTGRIAPDQWMLLVLDIFEDLPVGLFLACAYSOTLSTASTS 358
Qy 265 LMGVKDSNIHELEHEQEPFCASQMAEPFRTRDGVSYNQPVFLAGMGLAFYMTVLGF 324
Db 359 INAMAAVTVEDLIKPRMPGLAPR-----KLVFIS-KGLSFIY---GS 396
Qy 325 DCITTCYAVTQGLSGSILMSAGSAITG---IMGTV-----APT--WLRKRCGL--VR 371
Db 397 ACTLV-----AALSSILGGVQLGSGFTVMGVISGPLGARTLGMLLPACNTPGVL 446
Qy 372 TGLISGLAQLSCLILCVISVFMVPGSPDLVSPPFEDIRSRFTQGBSITPTKIPETITEY 431
Db 447 SGLAAGLA-VSLMWAVGATLYPPGE-----QTMGVLPFSAAGCTNDSV 488
Qy 432 M-----SNGSNSANIVPETSPE-----SVFIIISVLLFAGVIAARIGLSFDTLVTQLL 480
Db 489 LGGPGATNASGIPSSGMDTGRPALADTFYALSILYIGALG-----TLITML 536

RESULT 14

US-09-640-198D-4

; Sequence 4, Application US/09640198D
; Patent No. 6586411
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen
; APPLICANT: Kay Whye, Peng
; TITLE OF INVENTION: System for Monitoring the Location of
; TITLE OF INVENTION: Transgenes
; FILE REFERENCE: 07039-295001
; CURRENT APPLICATION NUMBER: US/09/640,198D
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-640-198D-4

Query Match 3.7%; Score 108; DB 4; Length 618;

Best Local Similarity 19.1%; Pred. No. 0.051;

Matches 103; Conservative 71; Mismatches 160; Indels 204; Gaps 27;

Qy 14 CGSLADYLTSAKFLLYGLHSLTWGDRMWHFAVSFLVELYGNLSLLLTAVYGLVAGSVL 73
Db 132 CGTL-QYLVAT--MLYTG-----IIVAPALILNQVTGLDIWASLL 169

Qy 74 VLGAIGDWVKNARLKVAQTSIVVQNVSVILCGIILMMVFLHKHELLTMYHGWL-LTSC 132
Db 170 STGIITLTLYTGGMKAVVWTD--VFQVVVMLVGF-----WILARG 209
Qy 133 YILIIITIANIANLATAITTIQ-----RDWIVVVG-----164
Db 210 VILGGPRNVLSLAQNHRSINLMDPDPDRSRYTFTWTFVGGTLVWLSMGVYQVQAQVRY 269
Qy 165 -----EDRSKLANMNATIRIDQLTNILAPMAVGQIMTFGSPVIGCGFTSGNLSVMCWE 219

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Db 270 VACHTEGKAKUALL-----NQQL-----GLFLIVASAAC-CG----- 300
QY 220 YVLLKVKYQK--TPALAVKAGLKEBETELKQNLHKDTEPKP-----LEGTH 264
Db 301 --INVVFYKDCDPLJTGRIAPDQYMPLLVDIFEDLPVPGFLACAYSGTLSTASTS 358
QY 265 LMGVKDSNIHELEHQBETFCASQMAEPRTFRDQWVSYYNQVFLAGMGLAFLNWTVLGP 324
Db 359 INAAVAATVEDLIKPRMFLAPR-----KLVFIS-KGLSFIY-----GS 396
QY 325 DCITTYGAYTQGLSGSILSLMGASAITG---IMGTV-----AFT--WLRKCGL--VR 371
Db 397 AGLTV-----AALSSLLGGVLOGSFTVMGVISGPLLGAFTLGMILLPACNTPCVL 445
QY 372 TGLISGLAQLSCLILCVISVFMGSPDLDSVSPEDIRSRFIOGESITPTKIPITTEIY 431
Db 447 SGLAAGLA-VSLWAVAGATLYPPGE-----QTMGVLPFTAAGCTNDVS 488
QY 432 M---SNGSNSANIVPETSPE-----SVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480
Db 489 LIGPGGATNAGSNGIFSSGMDTGRPALADTFYAISLYVYALG-----TUTWML 536

RESULT 15
US-09-543-681A-8251
; Sequence 8251, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8251
; LENGTH: 491
; TYPE: PRN
; ORGANISM: Proteus mirabilis
US-09-543-681A-8251

Query Match 3.7%; Score 107.5; DB 4; Length 491;
Best Local Similarity 19.7%; Pred. No. 0.039;
Matches 102; Conservative 68; Mismatches 152; Indels 197; Gaps 27;

QY 29 YLGHSLSTWGRMWHFA-----VSVELVELYGN-----LLLTAVYGLVWAGS----- 71
Db 28 YLIFSIELW-ERFGYGLQGINMAVYLVKMLGNSEAEAITVFAAFTALYGFVAIGWGLGD 86
QY 72 -----VLVLGAIIGDWVDKXNRLKVAQTSLVQNVSVILCGII----- 109
Db 87 KILGTFRVIVLGAIV-----LAIGYAMVAFSDHDKXVIYWGGLATIAVGNGLFKANPSS 139
QY 110 LMMVFLHKHE-----LLTWY-----HGWVLT---SCYILITIA 140
Db 140 LLATCYEKDDPOLDGAFWYVMSINVGSLMLATPWLAAANYGMDVAFALSVGVMILITLA 199
QY 141 NIANLASTATITIORDMIVVAGVDRSKLANMNAT--IRRIDQLTNIALPMAV----- 192
Db 200 N-----FNLRCGMI-----KDKSRDPDFELNYLKULLTLVGLVALTAVSTWLLH 244
QY 193 -QQIMTFGSPVIGCGFISGWNIV-----SMCEYEVLLWKYQKTP 231
Db 245 NNEVATWSLAIISLGI-----LIFARETFMMKGVARRKMIVAFLLMWAEAVVFFVLYDQMP 300
QY 232 ALAVKAGLKEEBETELKQNLHKDTEPKPLEGTHLGVKDSNIHELEH-----EQEPTCAS 286
Db 301 T-----SINFFA-----IHNVEHAILGFSVEP----- 322
QY 287 QMAEPRTFRDQWVSYYNQVFLAGMGLAFLNWTVLGDFCITTYGAYTQG--LSGSILSI 344
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Db 323 ---EQFQSLNPFW-----IMLASPLLAAY-NFMG-DKLEMPYKFTVGMFLSATAFLV 370
QY 345 LMGASAITGIMGTVAFTWLRKCGLVRTG--LIS--GLAQLSCLILCVISVFMGSPDL 400
Db 371 LPLGASMANEAGIVSSWMLVASVGFQSIGELMISGLGLAMVAQLVFORLGMGTIMGAWFLT 430
QY 401 SVSPFEDIRSRFIOGESITPTKIPE-----ITTEIYMS 433
Db 431 SAA-----AATAGKVASLMAVPEVDQNAHASLEIYSS 463
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Search completed: August 17, 2004, 18:08:36
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 18:04:06 ; Search time 50 Seconds
(without alignment)
3585.048 Million cell updates/sec

Title: US-09-715-927-6
Perfect score: 2929
Sequence: 1 MTRAGDHNRQCCGSLADY.....ACGPDKEVRKQNTSVV 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues
Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2929	100.0	571	15 US-10-341-434-169	Sequence 169, App
2	2929	100.0	571	15 US-10-331-496A-32	Sequence 32, Appl
3	2925	99.9	571	12 US-10/399	Sequence 2, Appli
4	2924	99.8	571	10 US-09-973-180-2	Sequence 2, Appli
5	2924	99.8	571	10 US-09-973-180-3	Sequence 3, Appli
6	2922	99.8	571	10 US-09-973-180-4	Sequence 4, Appli
7	2917	99.6	571	9 US-09-729-674-130	Sequence 130, App
8	2018	68.9	408	15 US-10-264-049-3007	Sequence 3007, Ap
9	1789	61.1	382	15 US-10-264-237-1491	Sequence 1491, Ap
10	1789	61.1	383	10 US-09-809-391-460	Sequence 460, App
11	1789	61.1	383	10 US-09-882-171-460	Sequence 460, App
12	1789	61.1	383	12 US-10-164-861-460	Sequence 460, App
13	656	22.4	484	16 US-10-437-963-157454	Sequence 157454,
14	605	20.7	511	12 US-10-425-114-67781	Sequence 67781, A
15	329	11.2	597	12 US-10-425-114-67278	Sequence 67278, A

16	318.5	10.9	552	16	US-10-437-963-134922	Sequence 134922,
17	285	9.7	587	12	US-10-424-599-195397	Sequence 195397,
18	271.5	9.3	593	16	US-10-437-963-122654	Sequence 122654,
19	248	8.5	159	12	US-10-424-599-269044	Sequence 269044,
20	188.5	6.4	150	12	US-10-424-599-221969	Sequence 221969,
21	171	5.8	129	12	US-10-424-599-271491	Sequence 271491,
22	126.5	4.3	523	15	US-10-099-322-122	Sequence 122, App
23	126.5	4.3	523	15	US-10-044-564-122	Sequence 122, App
24	126	4.3	529	12	US-10-403-161-36	Sequence 36, Appl
25	125.5	4.3	575	14	US-10-156-761-10350	Sequence 10350, A
26	124.5	4.3	523	15	US-10-099-322-123	Sequence 123, App
27	124.5	4.3	523	15	US-10-044-564-123	Sequence 123, App
28	124	4.2	529	12	US-10-403-161-38	Sequence 38, Appl
29	123.5	4.2	487	12	US-10-403-161-44	Sequence 44, Appl
30	123.5	4.2	524	12	US-10-403-161-34	Sequence 34, Appl
31	123.5	4.2	524	12	US-10-403-161-40	Sequence 40, Appl
32	123.5	4.2	524	12	US-10-403-161-42	Sequence 42, Appl
33	123.5	4.2	524	15	US-10-099-322-34	Sequence 34, Appl
34	123.5	4.2	524	15	US-10-099-322-121	Sequence 121, App
35	123.5	4.2	524	15	US-10-044-564-34	Sequence 34, Appl
36	123.5	4.2	524	15	US-10-044-564-121	Sequence 121, App
37	120	4.1	458	14	US-10-283-423-6	Sequence 6, Appli
38	120	4.1	458	14	US-10-213-821-6	Sequence 6, Appli
39	120	4.1	458	16	US-10-736-048-6	Sequence 6, Appli
40	119	4.1	537	9	US-09-738-626-6730	Sequence 6730, Ap
41	118.5	4.0	522	15	US-10-099-322-124	Sequence 124, App
42	118.5	4.0	522	15	US-10-044-564-124	Sequence 124, App
43	117.5	4.0	494	15	US-10-369-493-12526	Sequence 12526, A
44	114.5	3.9	424	9	US-09-738-626-3641	Sequence 3641, Ap
45	114.5	3.9	424	12	US-10-627-476-600	Sequence 600, App

ALIGNMENTS

RESULT 1
US-10-341-434-169
; Sequence 169, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-169

Query Match	100.0%	Score	2929	DB	15	Length	571
Best Local Similarity	100.0%	Pred. No.	1.7e-272				
Matches	571	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MTRAGDHNRQCCGSLADYLTSAKFLYLGHSLSTGDMHMFVSVFLVLYGNSLLL	60				
Db	1	MTRAGDHNRQCCGSLADYLTSAKFLYLGHSLSTGDMHMFVSVFLVLYGNSLLL	60				
QY	61	TAVYGLVAGSVLVGAIIGDWYDKNARKVAQTSLVVQVNSVILCGIILMVFLKHKL	120				
Db	61	TAVYGLVAGSVLVGAIIGDWYDKNARKVAQTSLVVQVNSVILCGIILMVFLKHKL	120				
QY	121	LTMYHGVNLSVCSYLIITITIANIANLASTATAITIQRDWIVVWVAGEDESKLANNATIRI	180				
Db	121	LTMYHGVNLSVCSYLIITITIANIANLASTATAITIQRDWIVVWVAGEDESKLANNATIRI	180				

181 DQTNILAPMAVQIMTFGSPVIGCGFISGWNLVSCVEYVLLWKVYQKTPALAVKAGLK 240
181 DQTNILAPMAVQIMTFGSPVIGCGFISGWNLVSCVEYVLLWKVYQKTPALAVKAGLK 240
241 EETELKQNLNKHDTBPKEPLGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
241 EETELKQNLNKHDTBPKEPLGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
301 SYNQVFLAGCLAFYMTVLGFCITTYAYTOGLSGSILSIILMGASAITGIMGTVP 360
301 SYNQVFLAGCLAFYMTVLGFCITTYAYTOGLSGSILSIILMGASAITGIMGTVP 360
361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQESITP 420
361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQESITP 420
421 TKIPEITTEIYNSNGSNSANIVPESVPIISVSLIFAGVIAARIGLWSDLTVTOLL 480
421 TKIPEITTEIYNSNGSNSANIVPESVPIISVSLIFAGVIAARIGLWSDLTVTOLL 480
481 QENVIESERGIINGVQNSNMNLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
481 QENVIESERGIINGVQNSNMNLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVW 571
541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVW 571

RESULT 2

US-10-331-496A-32
; Sequence 32, Application US/10331496A
; Publication No. US2003028305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014RI-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 32
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-32

Query Match 100.0%; Score 2929; DB 15; Length 571;
Best Local Similarity 100.0%; Pred. No. 1.7e-272;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTRAGDHNQRQCGCGSLADYLSAKFLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
DB 1 MTRAGDHNQRQCGCGSLADYLSAKFLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
QY 61 TAYGLVWAGSVLVLGAIIGDWVKNARKVACTSLVQNVSVILCGIILMMVFLHKLHEL 120
DB 61 TAYGLVWAGSVLVLGAIIGDWVKNARKVACTSLVQNVSVILCGIILMMVFLHKLHEL 120
QY 121 LTMHGWLTSCVILITITIANIANIASTATAITIQBDWIIVVAGEDRSKLANNNATIRI 180
DB 121 LTMHGWLTSCVILITITIANIANIASTATAITIQBDWIIVVAGEDRSKLANNNATIRI 180
QY 181 DQTNILAPMAVQIMTFGSPVIGCGFISGWNLVSCVEYVLLWKVYQKTPALAVKAGLK 240
DB 181 DQTNILAPMAVQIMTFGSPVIGCGFISGWNLVSCVEYVLLWKVYQKTPALAVKAGLK 240
QY 241 EETELKQNLNKHDTBPKEPLGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
DB 241 EETELKQNLNKHDTBPKEPLGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
QY 301 SYNQVFLAGCLAFYMTVLGFCITTYAYTOGLSGSILSIILMGASAITGIMGTVP 360
DB 301 SYNQVFLAGCLAFYMTVLGFCITTYAYTOGLSGSILSIILMGASAITGIMGTVP 360
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQESITP 420
DB 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQESITP 420
QY 421 TKIPEITTEIYNSNGSNSANIVPESVPIISVSLIFAGVIAARIGLWSDLTVTOLL 480
DB 421 TKIPEITTEIYNSNGSNSANIVPESVPIISVSLIFAGVIAARIGLWSDLTVTOLL 480
QY 481 QENVIESERGIINGVQNSNMNLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
DB 481 QENVIESERGIINGVQNSNMNLLDLHFTMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVW 571
DB 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVW 571

RESULT 3

US/10/399
; Sequence 2, Application US/10399488
; Publication No. US20040029147A1
; GENERAL INFORMATION:
; APPLICANT: Pietrangelo, Antonello
; TITLE OF INVENTION: Mutations in the ferroportin 1 gene associated with hereditary
; TITLE OF INVENTION: haemochromatosis
; FILE REFERENCE: 8907-097-999
; CURRENT APPLICATION NUMBER: US/10/399,488
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/EP01/12018
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: MI2000A002240
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (77)..(77)
; OTHER INFORMATION: The 'Xaa' at location 77 is either Asp or Ala depending on the va
US/10/399,488-2

Query Match

99.9%; Score 2925; DB 12; Length 571;

Best Local Similarity 99.8%; Pred. No. 4.1e-272;
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
Db 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120
Db 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120

QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180
Db 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

QY 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLSMCMVEYVLLMKVYQKTPALAVKAGLK 240
Db 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLSMCMVEYVLLMKVYQKTPALAVKAGLK 240

QY 241 EETELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEQPTCASOMAEPRFTFRDGVV 300
Db 241 EETELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEQPTCASOMAEPRFTFRDGVV 300

QY 301 SYNOPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSLMGASAITGIMGVAF 360
Db 301 SYNOPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSLMGASAITGIMGVAF 360

QY 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420
Db 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420

QY 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480
Db 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480

QY 481 QENVIESERGIINGVQNSNMNLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
Db 481 QENVIESERGIINGVQNSNMNLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

RESULT 4
US-09-973-180-2
; Sequence 2, Application US/09973180
; Publication No. US20030082553A1
; GENERAL INFORMATION:
; APPLICANT: Oestra, Ben Heutink, P Duijin, C.M.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOSIS
; FILE REFERENCE: 24594
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US/09/973,180
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 99.8%; Score 2924; DB 10; Length 571;
Best Local Similarity 99.8%; Pred. No. 5.2e-272;
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
Db 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120
Db 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120

QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180
Db 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

Db 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120
QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180
Db 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

QY 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLSMCMVEYVLLMKVYQKTPALAVKAGLK 240
Db 181 DQLTNILAPMAYGQIMTFGSPVIGCGFISGMNLSMCMVEYVLLMKVYQKTPALAVKAGLK 240

QY 241 EETELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEQPTCASOMAEPRFTFRDGVV 300
Db 241 EETELKQNLNKHDTPEKPLEGTHLMGVKDSNIHELEHEQPTCASOMAEPRFTFRDGVV 300

QY 301 SYNOPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSLMGASAITGIMGVAF 360
Db 301 SYNOPVFLAGMGLAFLYMTVLGFCITITGYAYTQGLSGSILSLMGASAITGIMGVAF 360

QY 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420
Db 361 TWIRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLDSVSPEDIRSRFIQGESITP 420

QY 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480
Db 421 TKIPEITTEIYMSNGSNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLL 480

QY 481 QENVIESERGIINGVQNSNMNLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
Db 481 QENVIESERGIINGVQNSNMNLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

RESULT 5
US-09-973-180-3
; Sequence 3, Application US/09973180
; Publication No. US20030082553A1
; GENERAL INFORMATION:
; APPLICANT: Oestra, Ben Heutink, P Duijin, C.M.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOSIS
; FILE REFERENCE: 24594
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US/09/973,180
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 99.8%; Score 2924; DB 10; Length 571;
Best Local Similarity 99.8%; Pred. No. 5.2e-272;
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60
Db 1 MTRAGDHNRRQCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

QY 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120
Db 61 TAYVGLVWAGSVLVLGAIIGDWDVKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120

QY 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180
Db 121 LTMVHGWLTSVYLLIITIANIANLASTATAITIQRDWIVVWVAGEDRSKLANMNATIRRI 180

Db 121 LTMHGWLTSCYIIITITANHAHLASTATATITORDWIVVAGEDRSKLANMATIRRI 180
QY 181 DQLTNILAPMAVGQIMTFGSPVIGGFTSGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240
Db 181 DQLTNILAPMAVGQIMTFGSPVIGGFTSGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240
QY 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
Db 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
QY 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMGTVA 360
Db 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMGTVA 360
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLSPEDIRSRFIQESITP 420
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLSPEDIRSRFIQESITP 420
QY 421 TKIPEITTEIYMSNGSANSIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTVTQL 480
Db 421 TKIPEITTEIYMSNGSANSIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTVTQL 480
QY 481 QENVIESERGIINGVQNSMNYLLDLHFTMVLAPNPEAFGLLVLSVSVFVANGHIMYFR 540
Db 481 QENVIESERGIINGVQNSMNYLLDLHFTMVLAPNPEAFGLLVLSVSVFVANGHIMYFR 540
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

RESULT 6
US-09-973-180-4
; Sequence 4, Application US/09973180
; Publication No. US2003082553A1
; GENERAL INFORMATION:
; APPLICANT: Oostera, Ben Heutink, P Duijin, C.M.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOSIS
; FILE REFERENCE: 24584
; CURRENT APPLICATION NUMBER: US/09/973,180
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/301,429
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 144
; OTHER INFORMATION: Xaa = any amino acid except Asp

US-09-973-180-4

Query Match 99.8%; Score 2922; DB 10; Length 571;
Best Local Similarity 99.8%; Pred. No. 8e-272;
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTRAGDHNQRCCGSLADYLTSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60
Db 1 MTRAGDHNQRCCGSLADYLTSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60
QY 61 TAVYGLWAGSVLVLAIGDWDVQAKLKAQTSLLVQNVSVILCGIILMWVFLHKHEL 120
Db 61 TAVYGLWAGSVLVLAIGDWDVQAKLKAQTSLLVQNVSVILCGIILMWVFLHKHEL 120
QY 121 LTMHGWLTSCYIIITITANHAHLASTATITORDWIVVAGEDRSKLANMATIRRI 180
Db 121 LTMHGWLTSCYIIITITANHAHLASTATITORDWIVVAGEDRSKLANMATIRRI 180
QY 181 DQLTNILAPMAVGQIMTFGSPVIGGFTSGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240

Db 181 DQLTNILAPMAVGQIMTFGSPVIGGFTSGMNLVSMCVYVLLWKVYQKTPALAVKAGLK 240
QY 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
Db 241 EETELKQNLNKHDTBPKEPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGV 300
QY 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMGTVA 360
Db 301 SYNQVFLAGMGLAFYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMGTVA 360
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLSPEDIRSRFIQESITP 420
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVMPGSPDLSPEDIRSRFIQESITP 420
QY 421 TKIPEITTEIYMSNGSANSIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTVTQL 480
Db 421 TKIPEITTEIYMSNGSANSIVPETSPEVPIISVSLFAGVIAARIGLWSPDLTVTQL 480
QY 481 QENVIESERGIINGVQNSMNYLLDLHFTMVLAPNPEAFGLLVLSVSVFVANGHIMYFR 540
Db 481 QENVIESERGIINGVQNSMNYLLDLHFTMVLAPNPEAFGLLVLSVSVFVANGHIMYFR 540
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

RESULT 7
US-09-729-674-130
; Sequence 130, Application US/09729674
; Patent No. US20010039335A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinhilber II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Pechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: (202)
; NAME/KEY: UNSURE
; LOCATION: (504)
; US-09-729-674-130

Query Match 99.6%; Score 2917; DB 9; Length 571;
Best Local Similarity 99.6%; Pred. No. 2.4e-271;
Matches 569; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRAGDHNQRCCGSLADYLTSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60
Db 1 MTRAGDHNQRCCGSLADYLTSAKFLYLGHSLSTWGRMWHFAVSFLVELYGNLSLL 60

QY 61 TAVYGLWAGSVLVGALIGDWDVKNARLKAQTSLVVQNVSVILCGIILMKVFLRHKL 120
Db 61 TAVYGLWAGSVLVGALIGDWDVKNARLKAQTSLVVQNVSVILCGIILMKVFLRHKL 120
QY 121 LTMVHGWLTSCYIIILITIANIANASTATAITIQDMLVIVVAGEDRSKLANMNTIRRI 180
Db 121 LTMVHGWLTSCYIIILITIANIANASTATAITIQDMLVIVVAGEDRSKLANMNTIRRI 180
QY 181 DQLTNILAPMAVGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLK 240
Db 181 DQLTNILAPMAVGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLK 240
QY 241 EEETELKQNLHKDTEPKPLEGTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGV 300
Db 241 EEETELKQNLHKDTEPKPLEGTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGV 300
QY 301 SYYNQPVFLAGMGLAFLYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMTVAF 360
Db 301 SYYNQPVFLAGMGLAFLYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMTVAF 360
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQGESITP 420
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQGESITP 420
QY 421 TKIPETITEIYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLWFSFDTLTQLL 480
Db 421 TKIPETITEIYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLWFSFDTLTQLL 480
QY 481 QENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
Db 481 QENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540
QY 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571
Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571

RESULT 8

US-10-264-049-3007
; Sequence 3007, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3007
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3007

Query Match 68.9%; Score 2018; DB 15; Length 408;
Best Local Similarity 100.0%; Pred. No. 4.6e-185;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 RIDQNTNILAPMAVGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAG 238
Db 16 RIDQNTNILAPMAVGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAG 75
QY 239 LKBEETELKQNLHKDTEPKPLEGTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDG 298
Db 76 LKBEETELKQNLHKDTEPKPLEGTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDG 135
QY 299 WVSYYNQPVFLAGMGLAFLYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMTV 358

Db 136 WVSYYNQPVFLAGMGLAFLYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMTV 195
QY 359 AFTWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQGESI 418
Db 196 AFTWLRKCGLVRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQGESI 255
QY 419 TPKIPETITEIYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLWFSFDTLTQ 478
Db 256 TPKIPETITEIYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLWFSFDTLTQ 315
QY 479 LLENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMY 538
Db 316 LLENVIESERGIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMY 375
QY 539 FRFAQNTLGNKLFACGPDPAKEVRKENQANTSVV 571
Db 376 FRFAQNTLGNKLFACGPDPAKEVRKENQANTSVV 408

RESULT 9

US-10-264-237-1491
; Sequence 1491, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1491
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1491

Query Match 61.1%; Score 1789; DB 15; Length 382;
Best Local Similarity 92.4%; Pred. No. 4.6e-163;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;
QY 190 MANGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLKEETELKQ 249
Db 1 MANGQIMTFGSPVIGCGFISGMNLVSMCVYVLLMKVYQKTPALAVKAGLKEETELKQ 60
QY 250 NLHKDTEPKPLEGTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGVSYNQPVFL 309
Db 61 NLHKDTEPKPLEGTHLMGVKDSNIHELEHQBPTCASQVABPRTFRDGVSYNQPVFL 120
QY 310 AGMGLAFLYMTVLGFCITTGAYTQGLSGSILSLMGASAITGIMTVAFWLKRCGL 369
Db 121 AGMGLAFLYMTVLGFCITTGAYTQGLSGFHPQYDFGSIYNNNGNSFYLATSKMFP 180
QY 370 VRTGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQGESITPKIPETITE 429
Db 181 GSAGLISGLAQLSCLILCVISVFMPSPLDLSVSPEDIRSRFIQGESITPKIPETITE 240
QY 430 IYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLWFSFDTLTQLLQENVIESER 489
Db 241 IYMSNGSNSANIVPETSPEVPIISVLLFAGVIAARIGLWFSFDTLTQLLQENVIESER 300
QY 490 GIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFRPAQNTLGNK 549
Db 301 GIINGVQNSMNYLLDLHFMVILAPNPEAFGLLVLSVSVFVAMGHIMYFRPAQNTLGNK 360
QY 550 LFACGPDPAKEVRKENQANTSVV 571
Db 361 LFACGPDPAKEVRKENQANTSVV 382

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RESULT 10
US-09-809-391-460
; Sequence 460, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (383)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-460

Query Match          61.1%; Score 1789; DB 10; Length 383;
Best Local Similarity 92.4%; Pred. No. 4.6e-163;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 MAVGQIMTFGSPVIGCGFISGWNLSMVEYVLLWKVYQKTPALAVKAGLKEEETELKQL 249
Db 1 MAVGQIMTFGSPVIGCGFISGWNLSMVEYVLLWKVYQKTPALAVKAGLKEEETELKQL 60
QY 250 NLHKOTEPKPLGTHLMGVKDSNIHELEHQEPTCASQVABPFRFRDQGWVSYNQPVFL 309
Db 61 NLHKOTEPKPLGTHLMGVKDSNIHELEHQEPTCASQVABPFRFRDQGWVSYNQPVFL 120
QY 310 AGWGLAFLVMTVLGFCITTGAYTQGLSGSILSMGASAITGIMGTVAFTLRRKQGL 369
Db 121 AGWGLAFLVMTVLGFCITTGAYTQGLSGSPFQDFGDSISVNNWNGSCSYLATSQWVF 180
QY 370 VRTGLISGLAQLSCLILCVISVMPGSLDLSVSPFDIRSRFQGESITPTKIPETITE 429
Db 181 GSAGLISGLAQLSCLILCVISVMPGSLDLSVSPFDIRSRFQGESITPTKIPETITE 240
QY 430 IYMSGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIIESER 489
Db 241 IYMSGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIIESER 300
QY 490 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLLVLSVSVFVAMGHIMYFRFAQNTLGK 549
Db 301 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLLVLSVSVFVAMGHIMYFRFAQNTLGK 360
QY 550 IFACGPDAAKEVRKENCANTSUV 571
Db 361 IFACGPDAAKEVRKENCANTSUV 382

RESULT 11
US-09-882-171-460
; Sequence 460, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (383)
; OTHER INFORMATION: Xaa equals stop translation
US-09-882-171-460

Query Match          61.1%; Score 1789; DB 10; Length 383;
Best Local Similarity 92.4%; Pred. No. 4.6e-163;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 MAVGQIMTFGSPVIGCGFISGWNLSMVEYVLLWKVYQKTPALAVKAGLKEEETELKQL 249
Db 1 MAVGQIMTFGSPVIGCGFISGWNLSMVEYVLLWKVYQKTPALAVKAGLKEEETELKQL 60
QY 250 NLHKOTEPKPLGTHLMGVKDSNIHELEHQEPTCASQVABPFRFRDQGWVSYNQPVFL 309
Db 61 NLHKOTEPKPLGTHLMGVKDSNIHELEHQEPTCASQVABPFRFRDQGWVSYNQPVFL 120
QY 310 AGWGLAFLVMTVLGFCITTGAYTQGLSGSILSMGASAITGIMGTVAFTLRRKQGL 369
Db 121 AGWGLAFLVMTVLGFCITTGAYTQGLSGSPFQDFGDSISVNNWNGSCSYLATSQWVF 180
QY 370 VRTGLISGLAQLSCLILCVISVMPGSLDLSVSPFDIRSRFQGESITPTKIPETITE 429
Db 181 GSAGLISGLAQLSCLILCVISVMPGSLDLSVSPFDIRSRFQGESITPTKIPETITE 240
QY 430 IYMSGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIIESER 489
Db 241 IYMSGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIIESER 300
QY 490 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLLVLSVSVFVAMGHIMYFRFAQNTLGK 549
Db 301 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLLVLSVSVFVAMGHIMYFRFAQNTLGK 360
QY 550 IFACGPDAAKEVRKENCANTSUV 571
Db 361 IFACGPDAAKEVRKENCANTSUV 382

PRIORITY FILING DATE: 1998-03-06
PRIORITY APPLICATION NUMBER: 60/040,162
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/040,333
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/038,621
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/040,626
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/040,334
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/040,336
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/040,163
PRIORITY FILING DATE: 1997-03-07
PRIORITY APPLICATION NUMBER: 60/047,600
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,615
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,597
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,502
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,633
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,583
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,617
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,618
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,503
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,592
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,581
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,584
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,500
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,587
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,492
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,598
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,613
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,582
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,596
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,612
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,632
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/047,601
PRIORITY FILING DATE: 1997-05-23
PRIORITY APPLICATION NUMBER: 60/043,580
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/043,568
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/043,314
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/043,569
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/043,311
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/043,671
PRIORITY FILING DATE: 1997-04-11
PRIORITY APPLICATION NUMBER: 60/043,674
PRIORITY FILING DATE: 1997-04-11
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PRIOR APPLICATION NUMBER: 60/043,669	PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,312	PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,313	PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,672	PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,315	PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/048,974	PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/056,886	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,877	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,889	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,893	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,530	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,878	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,562	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,872	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,882	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,637	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,903	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,888	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,879	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,880	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,894	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,911	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,636	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,874	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,910	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,864	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,631	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,845	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,892	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,761	PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/047,595	PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,599	PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,588	PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,590	PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,594	PRIOR FILING DATE: 1997-05-23

```
RESULT 12
US-10-164-861-460
; Sequence 460, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 460
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (383)
; OTHER INFORMATION: Xaa equals stop translation
US-10-164-861-460

Query Match 61.1%; Score 1789; DB 12; Length 383;
Best Local Similarity 92.4%; Pred. No. 4.6e-163;
Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

QY 190 MAVGQIMTFGSPVIGCGFISGNNLSMVCVEYVLLWKVYQKTPALAVKAGLKEEETELKQL 249
DB 1 MAVGQIMTFGSPVIGCGFISGNNLSMVCVEYVLLWKVYQKTPALAVKAGLKEEETELKQL 60
QY 250 NLHKTEPPLGTHLMGVKDSNIHELEHEOEFTCASQWABPFRFRDGTWYNNQPVFL 309
DB 61 NLHKTEPPLGTHLMGVKDSNIHELEHEOEFTCASQWABPFRFRDGTWYNNQPVFL 120
QY 310 AGMGLAFVMTVLGFDCTTGAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGL 369
DB 121 AGMGLAFVMTVLGFDCTTGAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGL 180
QY 370 VRTGLISGLAQLSCILCVISVFMPSGLDLSVSPFDIRSRFIQGESITPTKIPETITE 429
DB 181 GSAGLISGLAQLSCILCVISVFMPSGLDLSVSPFDIRSRFIQGESITPTKIPETITE 240
QY 430 IYMSNGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIESER 489
DB 241 IYMSNGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIESER 300
QY 490 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMYFPAONTLGNK 549
DB 301 GIINGVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMYFPAONTLGNK 360
QY 550 LPACGPDKEVRKQNKQANTSVV 571
DB 361 LPACGPDKEVRKQNKQANTSVV 382

RESULT 13
US-10-437-963-157454
; Sequence 157454, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 157454
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57023C.1.pap
US-10-437-963-157454

Query Match 22.4%; Score 656; DB 16; Length 484;
Best Local Similarity 29.9%; Pred. No. 6.8e-54;
Matches 157; Conservative 91; Mismatches 169; Indels 108; Gaps 8;

QY 28 LYLGHSLSTWGDWRMHFAVSVFLVELYGNLSLLLTAVYGLVAGSVLVLCALIGDWVDRNA 87
DB 27 LYVGHFLARWARMWFEFVGLYMRIRPGSLLLTAVYGVVEASAAALGPIYGAVDRLA 86
QY 88 RLKVAOTSLVQNVSVILCGIILMMVFLHKHLLTWYHGWLTSCVILLITIANI---A 143
DB 87 YLOVLRLLWLLQGSFVAAGSVTALLVYGARLAA--GF---PAFVALVVTNVYSGALA 141
QY 144 NLASTATATIORDWIVVVA--GEDRSKLANMATIRRIDQLNLIAPMAVGQIMTFGSPV 202
DB 142 ALSTLAGTILIEREWVVIAGGQPAAVLTGINSVIRRIDLSCKLLAPVLSGFFISFVSM 201
QY 203 ICGGFTISGNNLSMVCVEYVLLWKVYQKTPALAVKAGLKEEETELKQLNLHKTEPKLEG 262
DB 202 ASAAALAAWNLAAVWVQYVWLFVSVYAGFPAL-----SETQISRRADDDE---- 247
QY 263 THLMGVKDSNIHELEHEOEFTCASQWABPFRFR-----DGVSYNQVFLVLAGMG 313
DB 248 -----AAAAAQPKVERLMTMLPCWESWAVYARQEVVLPVGA 285
QY 314 LARLYMTVLGFDCTTGAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGLVRTG 373
DB 286 LARLYMTVLGFDCTTGAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGLVRTG 345
QY 374 LISGLAQLSCILCVISVFMPSGLDLSVSPFDIRSRFIQGESITPTKIPETITEIYMS 433
DB 346 LMSIWAQWCLLVCAVSWAGG----- 367
QY 434 NGNSANIVPETSPEVPIISVSLFAGVIAARIGLWSFDLTVTQLQENVIESERGIN 493
DB 368 -----AAPLASAMLMGGVAASRLGLMKPFDLAVMLQMDGVPESDRCVVG 412
QY 494 GVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMY 538
DB 413 GVQNSMNYLLDLHFIWILAPNPEAFGLLVLSVSVFAMGHIMY 457

RESULT 14
US-10-425-114-67781
; Sequence 67781, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
```

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; SEQ ID NO 67781
; LENGTH: 511
; TYPE: PR
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3632-036-H10_FLI pep
US-10-425-114-67781

Query Match
Best Local Similarity 20.7%; Score 605; DB 12; Length 511;
Matches 152; Conservative 103; Mismatches 186; Indels 98; Gaps 10;

Qy 13 CGSLADYLTSKFL--LVLHSLSTWGRMKHFAVSFLVELYCNLSLLTAVYGLVAVAG 70
Db 40 CSGS---PLDPIRLRYAGQILARWARMFEVSALYIMIRIPDSLFLFAIYGVETS 96
Qy 71 SVVLGAITGDVDRKARLKVAQTSVLVQNVSVILCGIILMMVFLHKLHLLTMVHGWL 130
Db 97 SLVVLGPVVTLVGRATYLVQLGWLSSQISLIVAGTAVTLLMYANLRATSF----- 150
Qy 131 SCYILITITIANI-----ANLSTATAITTDRIWVWV-AGEBRSKLANNNATIRIDQLTN 185
Db 151 PAFMALVATNVSGALAAALSALAGTILIEREWVVVISGHPSPSVRTGINSVVRIDLGCS 210
Qy 186 ILAPMAVGQIMTGPSPVIGCGPISGNVLSMCMVEYVLLWKVYQKTPALAVRAGLKEETE 245
Db 211 LLAPVLSALVISLASTQASAAVLALSTAASAGLQCLFVSVYNGVPALAAPQPRASDAE 270
Qy 246 LKQNLHKTDEPKLEGTHLMGVKDSNIHELEHEOEPTCA-----SMAEPPRTFR--DGW 299
Db 271 -----RPPVPMT-----VAPAAEAPTQALDWRARLADKLSVAGSWESW 309
Qy 300 VSYVNPVPLAGVLAFLYMTVLGFDCTITGVAYTQGLSGSILSLMGASAITGIMGTVA 359
Db 310 VYARQDVALPGVALAFLYFTVLSGTMTATLDWKGIPAYVISLARGFSAIVGIGATLL 369
Qy 360 FTWLRKCKGLVRTGLISGLAQLSCLILCVISVFMGSPDLDSVSPEDIRSRFIGESIT 419
Db 370 YPLVHRSVSTLRTGLWSIMWQCLLCVASVW----- 402
Qy 420 PKIKPEITTEIYMSGNSANIVPSPSPESVPIISVLSLLFAGVIAARIGLMSFDLTVTQL 479
Db 403 -----AATGASAWMLMAGVAASRLGLWTFDLAVNQL 434
Qy 480 LQENVIESRGIINGVQNSMNYLLDLHLHFIMVILAPNPEAFGLLLVLSVSVFVAGHIMY 538
Db 435 MQDGVDPDHERCVSVGVQNALQSVFDLLTVVAIVISDPKDFSKMIVLSFSLVTCAAWY 493

RESULT 15
US-10-425-114-67278
; Sequence 67278, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67278
; LENGTH: 597
; TYPE: PR
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4759-026-A6_FLI pep
US-10-425-114-67278
```

```
Query Match
Best Local Similarity 11.2%; Score 329; DB 12; Length 597;
Matches 125; Conservative 86; Mismatches 220; Indels 114; Gaps 14;

Qy 26 FLIYLGHSLSTWGRMKHFAVSFLVELYCNLSLLTAVYGLVAVAGSVLVLGAILGWDVK 85
Db 145 YALYASYLFGNLVEQLWNFAWPATLAILHPN--LLPVAIVGFFTKLSVFFGAPIVGKMDH 203
Qy 86 NARLKVQAQTSVLVQ--NVSVILCGIILMMVFLHKLHLLTMVHGWLTSYVILITIANIAN 144
Db 204 FPIPMYTALNAVQGTQLISAATVIYALRNLSHASTTAV---VLRPWFIALVAGAIER 260
Qy 145 LASTATAITTDRIWVWVAGEDRS--KLANNNATIRIDQLTNLTAMAVQIMTFPSPI 203
Db 261 LAGLGVSVRMDVWVLLAGTNRPVLAQANAVLNELDLVCEVSGASVFLGLLSKYHPVT 320
Qy 204 CGCFISGNVLSMCMVEYVLLWKVYQKTPALAVRAGLKEETEELKQLNLHKTDEPKPLEGT 263
Db 321 CLXIASGLMTCSP-----PVLVM-----LGQL----- 342
Qy 264 HLMGVKDSNIHELEHEQ-----EPTCASOM-----AEPPTFRDGWVSYYNQPVFLAGMG 313
Db 343 -----INRVSCHALDSRTATDESICADLLDVRRIIVENSRLAIKHGWNEYKQQTVLPSAA 398
Qy 314 LAFLYMTV--LGFDCTITGVAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCKGLVRT 372
Db 399 TVFENFVALAPGAILMTALLMHRGTSPSIVGAPSGLCISIMGLVATFISSLVKRVGILKA 458
Qy 373 GLISGLAQLSCLILCVISVFMGSPDLDSVSPEDIRSRFIGESITPKIKPEITTEIYM 432
Db 459 G-AAGLIFQASLLSIALTVYWAGS----- 481
Qy 433 SNGSNSANIVPSPSPESVPIISVLSLLFAGVIAARIGLMSFDLTVTQLLQENVIESRGI 492
Db 482 -----ISQTTPLLLIFLASIAL-----SRLGHMSYDVVVGTOIVQGVFASKANLI 525
Qy 493 NGVQNSMNYLLDLHLHFIMVILAPNPEAFGLLLVLSVSVFVAGHIMYFRAQNTLG--NKL 550
Db 526 GGMVSVIASLAELVMLAMAILIANDVSHFGFLAITSVSVAGAAWFMFCRWLTNFTDQREL 595
Qy 551 PACGP 555
Db 586 FMVDP 590

Search completed: August 17, 2004, 18:10:18
Job time : 52 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2004, 17:56:35 ; Search time 43 Seconds
(without alignments)
4189.788 Million cell updates/sec

Title: US-09-715-927-6

Perfect score: 2929

Sequence: 1 MTFAGDHNQRCCGSLADY.....ACGPDAKEVRKENQANTSVV 571

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_protein.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rviro.*
16: sp_bacterioph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2929	100.0	571	4 Q9NP59	Q9np59 homo sapien
2	2921	99.7	571	4 Q81VB2	Q81vb2 homo sapien
3	2906	99.2	571	4 Q9NRL0	Q9nrl0 homo sapien
4	2618	89.4	570	11 Q9JHI9	Q9jhi9 mus musculu
5	2612	89.2	570	11 Q9JHP4	Q9jhp4 mus musculu
6	2600	88.8	570	11 Q923U9	Q923u9 rattus norv
7	1975	5	562	13 Q9JFW0	Q9jfw0 brachydanio
8	1871	5	562	13 Q919R3	Q919r3 brachydanio
9	1894	5	528	13 Q9AW23	Q9aw23 brachydanio
10	1513	5	517	436 Q9AW28	Q9aw28 brachydanio
11	1479	5	50.5	405 Q921C9	Q921c9 rattus norv
12	1360	5	46.4	305 Q9EMES	Q9emes mus musculu
13	1021	5	34.9	13 Q9ZZS1	Q9zzs1 brachydanio
14	859	29.3	167	4 Q9NUS1	Q9nus1 homo sapien
15	677	23.1	133	4 Q724F8	Q724f8 homo sapien
16	612	20.9	524	10 Q80905	Q80905 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9NP59	PRELIMINARY;	PRT;	571 AA.
AC	Q9NP59;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Iron-regulated transporter IREG1 (Ferroporin) (Hypothetical protein)			
DE	(Solute carrier family 11 (Proton-coupled divalent metal ion			
DE	transporters), member 3).			
GN	IREG1 OR FPN1 OR DKPZP586J0624.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=20337919; PubMed=10882071;			
RA	McKie A.T., Marciani P., Rolfs A., Brennan K., Wehr K., Barrow D.,			
RA	Miret S., Bomford A., Peters I.J., Farzanen F., Hediger M.A.,			
RA	Hentze M.W., Simpson R.J.;			
RT	"A novel duodenal iron-regulated transporter, IREG1, implicated in the			
RL	basolateral transfer of iron to the circulation.";			
RL	Mol. Cell 5:299-309(2000).			
RC	[2]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=2015474; PubMed=10693807;			
RA	Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moyrihan J.,			
RA	Paw B.H., Drejer A., Barut B., Zapata A., Law T.C., Brugnara C.,			
RA	Lux S.E. IV, Pinkus G.S., Pinkus J.L., Kingsley P.D., Palis J.,			
RA	Fleming M.D., Andrews N.C., Zon L.I.;			
RT	"Positional Cloning of Zebrafish Ferroportin1 Identifies a Conserved			
RL	Vertebrate Iron Exporter.";			
RL	Nature 403:776-781(2000).			
RC	[3]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=10693807;			
RA	Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;			

Q9LZC8 arabidopsis
O44607 caenorhabdi
Q81A95 caenorhabdi
Q9BKT8 caenorhabdi
Q8BUM5 mus musculu
Q8W4E7 arabidopsis
O01891 caenorhabdi
O04629 arabidopsis
Q9JIM9 mus musculu
Q8G5T4 bifidobacte
Q81D64 bacillus ce
Q81G66 bacillus an
Q81PX7 bacillus an
Q81P57 bacillus an
Q8YIP3 ralatonia s
Q81CS3 bacillus ce
Q81BG3 bacillus ce
Q81D66 bacillus ce
Q9V6Z6 drosophila
Q82J22 streptomyce
Q97LU6 clostridium
Q8G2C7 brucella su
Q8YF15 brucella me
Q81P31 bacillus an
Q8G4V4 bifidobacte
Q8VNM1 drosophila
Q8S235 drosophila
Q81F48 bacillus ce
Q8FTZ6 corynebacte

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Strausberg R.;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF231121; AAF44330.1; -

DR EMBL; AF226614; AAF36697.1; -

DR EMBL; AL136944; CAB66878.1; -

DR EMBL; BC037733; AAH37733.1; -

DR Genew; HGNC:10909; SLCA0A1

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch carrier.

DR PROSITE; PS00215; MITOCH_CARRIER; 1.

KW Hypothetical protein.

SQ SEQUENCE 571 AA; 62542 MW; E4D6B5594C904959 CRC64;

Query Match 100.0%; Score 2929; DB 4; Length 571;
Best Local Similarity 100.0%; Pred. No. 8.7e-220;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRAGDHNQRGCCGLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

Db 1 MTRAGDHNQRGCCGLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

Qy 61 TAYGLVWAGSVLVGAIIGDWVKNARKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

Db 61 TAYGLVWAGSVLVGAIIGDWVKNARKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

Qy 121 LTMHGWLTSCVILITITANTANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

Db 121 LTMHGWLTSCVILITITANTANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

Qy 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

Db 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

Qy 241 EEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGMV 300

Db 241 EEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGMV 300

Qy 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTITGYAYTQGLSGSILSLMGASAITGIMGTVA 360

Db 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTITGYAYTQGLSGSILSLMGASAITGIMGTVA 360

Qy 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLDSVPEDIRSRFIQGESITP 420

Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLDSVPEDIRSRFIQGESITP 420

Qy 421 TKIPEITTEIYNSNGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLVTQTLL 480

Db 421 TKIPEITTEIYNSNGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLVTQTLL 480

Qy 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

Db 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

Qy 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

RESULT 2

Q81VB2

ID Q81VB2 PRELIMINARY; PRT; 571 AA.

AC Q81VB2

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Solute carrier family 11 (Proton-coupled divalent metal ion

DE transporters), member 3.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC035893; AAH35893.1; -

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch carrier.

DR PROSITE; PS00215; MITOCH_CARRIER; 1.

SQ SEQUENCE 571 AA; 62482 MW; 45D6B5503C90495F CRC64;

Query Match 99.7%; Score 2921; DB 4; Length 571;
Best Local Similarity 99.8%; Pred. No. 3.7e-219;
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTRAGDHNQRGCCGLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

Db 1 MTRAGDHNQRGCCGLADYLSAKFLLYLGHSLSTWGDMMHFAVSFLVELYGNLSLL 60

Qy 61 TAYGLVWAGSVLVGAIIGDWVKNARKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

Db 61 TAYGLVWAGSVLVGAIIGDWVKNARKVAQTSLVQNVSVILCGIILMMVFLKHHEL 120

Qy 121 LTMHGWLTSCVILITITANTANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

Db 121 LTMHGWLTSCVILITITANTANLASTATAITIQDWMIVVAGDRSKLANNTATIRI 180

Qy 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

Db 181 DQLTNLLAPMAVQIMTFGSPVIGCGFISGMNLVSMCEYVLLWKVYQKTPALAVKAGLK 240

Qy 241 EEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGMV 300

Db 241 EEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGMV 300

Qy 301 SYNQVQVFLAGMGLAFLYMTVLGFDCTITGYAYTQGLSGSILSLMGASAITGIMGTVA 360

Db 301 SYNQVQVFLAGMGLAFLYMTVLGSDCTITGYAYTQGLSGSILSLMGASAITGIMGTVA 360

Qy 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLDSVPEDIRSRFIQGESITP 420

Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVPMGSPDLDSVPEDIRSRFIQGESITP 420

Qy 421 TKIPEITTEIYNSNGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLVTQTLL 480

Db 421 TKIPEITTEIYNSNGNSANIVPESPESVPIISVSLFAGVIAARIGLWSPDLVTQTLL 480

Qy 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

Db 481 QENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSVSVFVAMGHIMYFR 540

Qy 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

Db 541 FAQNTLGNKLFACGPDPAKEVRKENQANTSV 571

RESULT 3

Q9NRLO

ID Q9NRLO PRELIMINARY; PRT; 571 AA.

AC Q9NRLO

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE SCLIA3 iron transporter.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347902; PubMed=10747949;
RA Abboud S., Haile D.J.;
RT "A Novel Mammalian Iron-regulated Protein Involved in Intracellular
RT Iron Metabolism.";
RL J. Biol. Chem. 275:19906-19912(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20291023; PubMed=10828623;
RA Haile D.J.;
RT "Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to
RT human chromosome 2q32 by in situ hybridization.";
RL EMBL; AF215636; AAF80986.1; -.
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0005887; C.integral to plasma membrane; TAS.
DR GO; GO:0005381; P.ferron ion transporter activity; TAS.
DR GO; GO:0007345; P.embryogenesis and morphogenesis; TAS.
DR GO; GO:0006879; P.ferron ion homeostasis; TAS.
DR GO; GO:0006826; P.ferron ion transport; TAS.
DR InterPro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 571 AA; 62581 MW; 89707BFFC4A4B921 CRC64;
Query Match 99.2%; Score 2906; DB 4; Length 571;
Best Local Similarity 99.5%; Pred. No. 5.4e-218;
Matches 568; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MTRAGDHNQRCGCCSLADYLTSAFLYLGHSLSTGDRMWHFAVSFLVELYCNLSLL 60
Db 1 MTRAGDHNQRCGCCSLADYLTSAFLYLGHSLSTGDRMWHFAVSFLVELYCNLSLL 60
QY 61 TAVYGLVAGSVLVLGAIIGDWDVXNARLKVAQTSILVQNVSVILCGILMMVFLKHEL 120
Db 61 TAVYGLVAGSVLVLGAIIGDWDVXNARLKVAQTSILVQNVSVILCGILMMVFLKHEL 120
QY 121 LTMVHGVLTSCVILLIITANTANLASTATITQIDMIWVVGDRSKLANMATIIRI 180
Db 121 LTMVHGVLTSCVILLIITANTANLASTATITQIDMIWVVGDRSKLANMATIIRI 180
QY 181 DQLTNLAPVAGQVMTFSGPVIGCGFSGWNLVSMVCEYVLLWKVYQKTPALAVKAGLK 240
Db 181 DQLTNLAPVAGQVMTFSGPVIGCGFSGWNLVSMVCEYVLLWKVYQKTPALAVKAGLK 240
QY 241 EBETELKQLNLHKDTEPKPLEGTHLGVKDSNIHELEHEQEPTCASQMAEPFRDQGW 300
Db 241 EBETELKQLNLHKDTEPKPLEGTHLGVKDSNIHELEHEQEPTCASQMAEPFRDQGW 300
QY 301 SYNOPVFLAGVGLAFVMTVLGPDCTTGAYATGGLSGSILSLMGASAITGIMGVAF 360
Db 301 SYNOPVFLAGVGLAFVMTVLGPDCTTGAYATGGLSGSILSLMGASAITGIMGVAF 360
QY 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMFGSPDLSPEDIRSRFIQGESITP 420
Db 361 TWLRKCGLVRTGLISGLAQLSCLILCVISVFMFGSPDLSPEDIRSRFIQGESITP 420
QY 421 TKIPEITTHIYNSGNSANIPTSPSPVPIISVSLFPAGVIAIRIGLWFDLTVTQLL 480
Db 421 TKIPEITTHIYNSGNSANIPTSPSPVPIISVSLFPAGVIAIRIGLWFDLTVTQLL 480
QY 481 QENVIESERGIINGVQNSMNYLLDLHFTIMVILANPEAFGLLVLISVSFVAMGHIMYFR 540
Db 481 QENVIESERGIINGVQNSMNYLLDLHFTIMVILANPEAFGLLVLISVSFVAMGHIMYFR 540
QY 541 FQNTLGNKLPACGPDPAKVEVRKENQANTSVV 571
Db 541 FQNTLGNKLPACGPDPAKVEVRKENQANTSVV 571
RESULT 4
Q9JHI9
AC NCBI_TaxID=9606; PRELIMINARY; PRT; 570 AA.
Q9JHI9
01-OCT-2000 (T-EMBLrel. 15, Created)
01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
01-OCT-2000 (T-EMBLrel. 25, Last annotation update)
DE SLC11A3 iron transporter (Ferroportin) (Solute carrier family 39
DE (iron-regulated transporter), member 1).
GN SLC40A1 OR FPN1 OR SLC39A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347902; PubMed=10747949;
RA Abboud S., Haile D.J.;
RT "A Novel Mammalian Iron-regulated Protein Involved in Intracellular
RT Iron Metabolism.";
RL J. Biol. Chem. 275:19906-19912(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20291023; PubMed=10828623;
RA Haile D.J.;
RT "Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to
RT human chromosome 2q32 by in situ hybridization.";
RL Cytogenet. Cell Genet. 88:328-329(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
MEDLINE=20155474; PubMed=10693807;
Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moynihan J.,
Paw B.H., Drejer A., Barut B., Zapata A., Law T.C., Brugnara C.,
Lux S.E. IV, Pinkus G.S., Pinkus J.L., Kingsley P.D., Pallas J.,
Fleming M.D., Andrews N.C., Zon L.I.;
RT "Positional Cloning of Zebrafish Ferroportin1 Identifies a Conserved
RT Vertebrate Iron Exporter.";
RL Nature 403:776-781(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=21085650; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa K., Iwata M., Nishi K., Kiyosawa H., Kondo J., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrinel L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF215637; AAF80987.1; -.
EMBL; AF226613; AAF36696.1; -.
EMBL; AK008700; BAE25840.1; -.
EMBL; BC003438; AAH03438.1; -.
EMBL; MGI:1315204; SLC40a1.
DR GO; GO:0005381; P.ferron ion transporter activity; IDA.
DR GO; GO:0006826; P.ferron ion transport; IDA.
DR InterPro; IPR001993; Mitoch carrier.

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DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 570 AA; 62702 MW; 7125CC66171394A0A CRC64;

Query Match      89.4%; Score 2618.5; DB 11; Length 570;
Best Local Similarity 90.2%; Pred. No. 1.4e-195;
Matches 518; Conservative 18; Mismatches 31; Indels 7; Gaps 3;

QY 1 MTRAGDHNQRCCGSLADYLTSAKFLYLGHSLSTWGRMMHFAVSFLVELYGNLSLL 60
   |||||
DB 1 MTKARDQTHQEGCCGSLANLYLSAKFLYLGHSLSTWGRMMHFAVSFLVELYGNLSLL 60
   |||||
QY 61 TAVYGLVWAGSVLVLCALIGDWVKNARKVAQTSLVQVNSVILCGIILMMVFLHKEEL 120
   |||||
DB 61 TAVYGLVWAGSVLVLCALIGDWVKNARKVAQTSLVQVNSVILCGIILMMVFLHKNEL 120
   |||||
QY 121 LTMHGWLTSCVILITITANTANLASTATATITORDWIVVAGEDRSKLANMATIRRI 180
   |||||
DB 121 LTMHGWLTSCVILITITANTANLASTATATITORDWIVVAGENRSLADMATIRRI 180
   |||||
QY 181 DQTNILAPWAGQIMTFGSPVIGCGFISGMNLVSMCVYVLLWKVYOKTPALAVKAGLK 240
   |||||
DB 181 DQTNILAPWAGQIMTFGSPVIGCGFISGMNLVSMCVYVLLWKVYOKTPALAVKALK 240
   |||||
QY 241 EETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGMV 300
   |||||
DB 241 VBESELKQLTSPKDTPEKPLEGTHLMGEKDSNIRELECEQEPTCASQMAEPFRTRDGMV 300
   |||||
QY 301 SYNQVFLAGMGLAFVLYMTVIGFCITTGAYATQGLSGSILSLIMGASAITGIMGTVA 360
   |||||
DB 301 SYNQVFLAGMGLAFVLYMTVIGFCITTGAYATQGLSGSILSLIMGASAITGIMGTVA 360
   |||||
QY 361 TWLRRKCGLVRTGLISGLAQLSCLILCVISVPMPSPLDLSVPPEDIRSRFIQGESITP 420
   |||||
DB 361 TWLRRKCGLVRTGLISGLAQLSCLILCVISVPMPSPLDLSVPPEDIRSRFVNPVSP 420
   |||||
QY 421 -TKIPE--ITTELYMSGNSANIPEPSPESVPIISVLSLLFAGVIAARIGLWSPDLTVT 477
   |||||
DB 421 TTKIPETVFTTEMHMSNMNSN----VHEMSTKPIPIVSLSLLFAGVIAARIGLWSPDLTVT 476
   |||||
QY 478 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 537
   |||||
DB 477 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 536
   |||||
QY 538 YRFAQNTLGNKLFACGPDPAKVRKENQNTSVV 571
   |||||
DB 537 YRFAQNTLGNQIFVCGPDEKEVTQNTSVV 570
   |||||

RESULT 5
Q9JPK4 PRELIMINARY; PRT; 570 AA.
AC Q9JPK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Iron-regulated transporter IREG1.
GN SLC40A1 OR SLC39A1 OR IREG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2037919; PubMed=10882071;
RA McKie A.T., Marciani P., Rolfs A., Brennan K., Wehr K., Barrow D.,
RA Miret S., Bomford A., Peters T.J., Farzaneh F., Hediger M.A.,
RA Hentze M.W., Simpson R.J.;
RT "A novel duodenal iron-regulated transporter, IREG1, implicated in the
RT basolateral transfer of iron to the circulation.";
RL Mol. Cell 5:293-309(2000).
DR EMBL; AF231120; AAF44329.1; --
DR MGD; MGI:1315204; SLC40A1.
DR GO; GO:0005381; F:iron ion transporter activity; IDA.

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DR GO; GO:0006826; P:iron ion transport; IDA.
DR IncePro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR SQ SEQUENCE 570 AA; 62656 MW; C648A6C61C51EDCD CRC64;

Query Match      89.2%; Score 2612.5; DB 11; Length 570;
Best Local Similarity 90.1%; Pred. No. 4.1e-195;
Matches 517; Conservative 18; Mismatches 32; Indels 7; Gaps 3;

QY 1 MTRAGDHNQRCCGSLADYLTSAKFLYLGHSLSTWGRMMHFAVSFLVELYGNLSLL 60
   |||||
DB 1 MTKARDQTHQEGCCGSLANLYLSAKFLYLGHSLSTWGRMMHFAVSFLVELYGNLSLL 60
   |||||
QY 61 TAVYGLVWAGSVLVLCALIGDWVKNARKVAQTSLVQVNSVILCGIILMMVFLHKEEL 120
   |||||
DB 61 TAVYGLVWAGSVLVLCALIGDWVKNARKVAQTSLVQVNSVILCGIILMMVFLHKNEL 120
   |||||
QY 121 LTMHGWLTSCVILITITANTANLASTATATITORDWIVVAGEDRSKLANMATIRRI 180
   |||||
DB 121 LTMHGWLTSCVILITITANTANLASTATATITORDWIVVAGENRSLADMATIRRI 180
   |||||
QY 181 DQTNILAPWAGQIMTFGSPVIGCGFISGMNLVSMCVYVLLWKVYOKTPALAVKAGLK 240
   |||||
DB 181 DQTNILAPWAGQIMTFGSPVIGCGFISGMNLVSMCVYVLLWKVYOKTPALAVKALK 240
   |||||
QY 241 EETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTRDGMV 300
   |||||
DB 241 VBESELKQLTSPKDTPEKPLEGTHLMGEKDSNIRELECEQEPTCASQMAEPFRTRDGMV 300
   |||||
QY 301 SYNQVFLAGMGLAFVLYMTVIGFCITTGAYATQGLSGSILSLIMGASAITGIMGTVA 360
   |||||
DB 301 SYNQVFLAGMGLAFVLYMTVIGFCITTGAYATQGLSGSILSLIMGASAITGIMGTVA 360
   |||||
QY 361 TWLRRKCGLVRTGLISGLAQLSCLILCVISVPMPSPLDLSVPPEDIRSRFIQGESITP 420
   |||||
DB 361 TWLRRKCGLVRTGLISGLAQLSCLILCVISVPMPSPLDLSVPPEDIRSRFVNPVSP 420
   |||||
QY 421 -TKIPE--ITTELYMSGNSANIPEPSPESVPIISVLSLLFAGVIAARIGLWSPDLTVT 477
   |||||
DB 421 TTKIPETVFTTEMHMSNMNSN----VHEMSTKPIPIVSLSLLFAGVIAARIGLWSPDLTVT 476
   |||||
QY 478 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 537
   |||||
DB 477 QLLQENVIESERGIINGVQNSMNYLLDLHFTWVILAPNPEAFGLLVLSISFVAMGHIM 536
   |||||
QY 538 YRFAQNTLGNKLFACGPDPAKVRKENQNTSVV 571
   |||||
DB 537 YRFAQNTLGNQIFVCGPDEKEVTQNTSVV 570
   |||||

RESULT 6
Q923U9 PRELIMINARY; PRT; 570 AA.
AC Q923U9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferroportin 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RA Yeh K.-Y., Yeh M., Glass J.;
RT "Iron induces ferroportin 1 (Fp1) clustering and redistribution in
RT rat intestinal epithelial cells.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394785; AAK77858.2; --
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.

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DR InterPro; IPR001993; Mitoch_carrier.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 570 AA; 62586 MW; 766786P22P054E94 CRC64;

Query Match      88.8%; Score 2600.5; DB 11; Length 570;
Best Local Similarity 89.9%; Pred. No. 3.5e-194;
Matches 514; Conservative 19; Mismatches 36; Indels 3; Gaps 2;

QY 1 MTRAGDHNQRGCGSLADYLSAKFLLYLGHSLSTWGDMMHFAVSVFLVELYGNLSLL 60
DB 1 MTKSRDQTHQEGCGSLANLYLSAKFLLYLGHSLSTWGDMMHFAVSVFLVELYGNLSLL 60
QY 61 TAYGLVAVAGSVLVLGAILGDWVDKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLH 120
DB 61 TAYGLVAVAGSVLVLGAILGDWVDKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLH 120
QY 121 LTMHGVNLTSCYILITITIANIANLASTATAITIQDWTIVVAGBDRSKLANNNATIRRI 180
DB 121 LNMVHGWLTVCVILITITIANIANLASTATAITIQDWTIVVAGBDRSKLANNNATIRRI 180
QY 181 DQNTNILAPMAVGQIMTFGSPVIGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLK 240
DB 181 DQNTNILAPMAVGQIMTFGSPVIGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLK 240
QY 241 EEETELKQNLNKHDTSPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGMV 300
DB 241 VESEELKQLTSPKDIPEKPLEGTHLMGEKDSNIHELECEQEPTCASQIAEPRTFRDGMV 300
QY 301 SYNQPVFLAGMLAFYMTVLGFCITITGYAYTOGLSGSILSLMGASAITGIMGTAVF 360
DB 301 SYNQPVFLAGMLAFYMTVLGFCITITGYAYTOGLSGSILSLMGASAITGIMGTAVF 360
QY 361 TWLRKCGAVRTGLISGLAQLSCLLCVLSVMPGSPDLSPEDRSRPIQEST-T 419
DB 361 TWLRKCGAVRTGLISGLAQLSCLLCVLSVMPGSPDLSPEDRSRPIHEEAVSS 420
QY 420 PTXKIPITTEIYMSNGSANSIVPETSPEVPIISVLLFAGVIAARIGLWSFDLTVTQL 479
DB 421 TTKIPE--TEMLMSNVSVNVTHEMSTKSVPIISVLLFAGVIAARIGLWSFDLTVTQL 478
QY 480 LQENVIESRGIINGVQNSMNYLLDLHFIMVILAPNPEAFGLLVLSVSVFVAMGHIMYP 539
DB 479 LQENVIESRGIINGVQNSMNYLLDLHFIMVILAPNPEAFGLLVLSVSVFVAMGHIMYP 538
QY 540 RFAQNTLGNKLPACGPDACEVRKENCQNTSVV 571
DB 539 RFAQNTLGNQIFVCAPDEKEVDESQNTSVV 570

RESULT 7
Q8JFWO PRELIMINARY; PRT; 562 AA.
AC Q8JFWO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SI:d22i1013.7 (Solute carrier family 39 (Iron-regulated transporter), member 1).
DE NCBI_TaxID=7955;
GN SLC39A1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Babbage A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL591593; CAD43474.1; -.
SQ SEQUENCE 562 AA; 61761 MW; 35CB30971553718F CRC64;

Query Match      67.4%; Score 1975.5; DB 13; Length 562;
Best Local Similarity 71.0%; Pred. No. 1.8e-145;

Matches 394; Conservative 64; Mismatches 72; Indels 25; Gaps 10;

QY 14 CGSLADYLSAKFLLYLGHSLSTWGDMMHFAVSVFLVELYGNLSLLTAVYGLVAVAGSVL 73
DB 11 CERPREFFKSAKFLIIVGHSLSTWGDMMHFAVSVFLVELYGNLSLLTAVYGLVAVAGSVL 70
QY 74 VLGAIGDWDVDKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLHLLTMHGVNLTSCY 133
DB 71 LGAIGDWDVDKNARKLVKVAQTSLVVQVNSVILCGIILMMVFLHKLHLLTMHGVNLTSCY 130
QY 134 ILITITIANIANLASTATAITIQDWTIVVAGBDRSKLANNNATIRRIDQNTNILAPMAVG 193
DB 131 IMWISITIANIANLASTATAITIQDWTIVVAGBDRSKLANNNATIRRIDQNTNILAPMAVG 190
QY 194 QIMTFGSPVIGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGLKE-EETELKQNLN 252
DB 191 QIMAFGSHFICGCGFISGNLVSVCVEYFLWKVYQKTPALAVKAGKDDQELKHLNIQ 250
QY 253 KD---TEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPRTFRDGMVSVYVQVFL 309
DB 251 KEIGNTE-SPVEASQLM-----TESSEPKDKTCCYQMAEPIRTFKDGMVAYVYVQSIFF 303
QY 310 AGMLAFYMTVLGFCITITGYAYTOGLSGSILSLMGASAITGIMGTAVFTWLRKCGL 369
DB 304 AGMLAFYMTVLGFCITITGYAYTOGLSGSVLSLLMGASAVSGICGTAVFTWIRKCGL 363
QY 370 VRTGLISGLAQLSCLLCVLSVMPGSPDLSPEDRSRPIQGES-----ITPKIPE 425
DB 364 IRTGFIAGVTQLSCLLCVASVPAGSPFDLSVPFEEV-LRHLFGDSGLRESPTFIP- 421
QY 426 ITTEIYMSNGSANSI-VPEPSPESVPIISVLLFAGVIAARIGLWSFDLTVTQLQENV 484
DB 422 -TTPEPI-----QANTVFEAPVESYMSVGLLFGVIAARVGLWSFDLTVTQLQENV 475
QY 485 IESERGIINGVQNSMNYLLDLHFIMVILAPNPEAFGLLVLSVSVFVAMGHIMYFPAQN 544
DB 476 IESERGIINGVQNSMNYLLDLHFIMVILAPNPEAFGLLVLSVSVFVAMGHIMYFPAQN 535
QY 545 TLGNKFLA-CGPDAX 558
DB 536 SLGSRUFLFCSPQK 550

RESULT 8
Q919R3 PRELIMINARY; PRT; 562 AA.
AC Q919R3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ferroportin.
GN SLC39A1 OR FPN1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=20155474; PubMed=10693807;
RA Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moynihan J.,
RA Paw B.H., Drejer A., Barut B., Zapata A., Law T.C., Brugnara C.,
RA Lux S.E. IV, Pinkus G.S., Pinkus J.L., Kingsley P.D., Palis J.,
RA Fleming M.D., Andrews N.C., Zon L.I.;
RP "Positional Cloning of Zebrafish Ferroportin1 Identifies a Conserved
RP Vertebrate Iron Exporter.";
RL Nature 403:776-781(2000).
DR EMBL; AF226612; AAF36695.1; -.
SQ ZFIN; ZDB-GENE-000511-8; slc39a1.
SQ SEQUENCE 562 AA; 61760 MW; 38A6838E2107FBAF CRC64;

Query Match      67.3%; Score 1971.5; DB 13; Length 562;

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QY 306 PVFLAGMGLAFLYMTVLGPDCTTGYAYTQGLSGSILSLMGASAITGIMGTVAFTWLR 365
Db 174 SIFPAGMSLAFLYMTVLGPDCTTGYAYTQGLSGSILSLMGASAVSGICQVFTWIRK 233
QY 366 KQGLVRTGLISGLAQLSCLILCVISVFMFGPGLDLSVSPFFEDIRSRFIOGESITP 421
Db 234 KQGLRTGTGFIAGVTQLSCLTLCVAVFAPGPFDLVSVPFEV-LRHLFGDSGSLRESPT 292
QY 422 KPIETTEIYMGNGNSANI-VPEISPSVPIISVLLFAGVIAARIGLMSFDTLVTQLL 480
Db 293 FIP--TTEPPI-----QANVTVEAPPVESYMSVGLLFAGVIAARVGLMSFDTLVTQLI 345
QY 481 QENVIESERGIINGVQNSMNYLLDLHLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFR 540
Db 346 QENVIESERGVINGVQNSMNYLLDLHLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFR 405
QY 541 FAQNTLGNKFLA-CGPDAK 558
Db 406 FAYKSLGSLRFLFCGPEQK 424
RESULT 11
Q921C9 PRELIMINARY; PRT; 405 AA.
AC Q921C9;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
DE Call adhesion regulator.
GN CARL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang X.Z.; (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-1996); AAD00260.1; -
DR EMBL; U76714; AAD00260.1; -
SQ SEQUENCE 405 AA; 45145 MW; ABDF5916C43AA4DA CRC64;

Query Match 50.5%; Score 1479.5; DB 11; Length 405;
Best Local Similarity 78.4%; Pred. No. 5.5e-107;
Matches 298; Conservative 15; Mismatches 36; Indels 31; Gaps 4;
QY 1 MTRAGDNRQRCCGSLADYLSAKFLYLGHSLSTWGDMMHFAVSFVLVELYNSLL 60
Db 1 MTKSRDQTHQEGCGGSLANVLSAKFLYLGHSLSTWGDMMHFAVSFVLVELYNSLL 60
QY 61 TAVYGLVWAGSVLVGAILGDWVDKNARKVAQTSLVYQNSVILCGIILAMVFLKHKL 120
Db 61 TAVYGLVWAGSVLVGAILGDWVDKNARKVAQTSLVYQNSVILCGIILAMVFLKHKL 120
QY 121 LTMVHGWLTSVYLITITIANIANLASTATITIQDWTIVVAVGDRSKLANMATIRRI 180
Db 121 LNMVHGWLTVCYLITITIANIANLASTATITIQDWTIVVAVGDRSKLANMATIRRI 180
QY 181 DQNTILAPMAGQIMTFGSPVIGCGFTSGWNLVSMCVBYLLMKYOKTALAVKAGLK 240
Db 181 DQNTILAPMAGQIMTFGSPVIGCGFTSGWNLVSMCVBYLLMKYOKTALAVKAGLK 240
QY 241 EEETELKQLNLHKDTEPKLEGTHLMGVKDSNIHEHEOEPTCASQMAEPFRPDGWV 300
Db 241 VEESELKQLTSKPDTEPKLEGTHLMGVKDSNIHEHEOEPTCASQMAEPFRPDGWV 300
QY 301 SYYNQPVFLAGMGLAF-----LYMTVLGDCITTT--YAYTQGLSGSILSLMGAS 349
Db 301 SYYNQPVFLAGMGLAGPGLYDPSGLRLYRHSI---CLHSGTEFWHFQPCDGSISN----- 351
QY 350 AITGIMGTVAFTWLRKCGL 369
Db 352 -----NMNNGNCGL 360

RESULT 12
Q8BME5 PRELIMINARY; PRT; 305 AA.
AC Q8BME5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Solute carrier family 39
GN SLC40A1 OR SLC39A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK032732; BAC28001.1; -
DR MGD; MGI:1315204; SLC40A1.
DR GO; GO:0005381; P:Iron ion transporter activity; IDA.
DR GO; GO:0006826; P:Iron ion transport; IDA.
DR InterPro; IPR001993; Mitoch carrier.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
SQ SEQUENCE 305 AA; 33574 MW; EC9FE6264AF4D887 CRC64;

Query Match 46.4%; Score 1360.5; DB 11; Length 305;
Best Local Similarity 88.0%; Pred. No. 7.2e-98;
Matches 272; Conservative 11; Mismatches 19; Indels 7; Gaps 3;
QY 266 MGVDKSNHLEHEOEPTCASQMAEPFRTRFDGWVSYNQPVFLAGMGLAFLYMTVLGFD 325
Db 1 MGEKDSNIRELECEQEPTCASQMAEPFRTRFDGWVSYNQPVFLAGMGLAFLYMTVLGFD 60
QY 326 CITTGYAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQLSCL 385
Db 61 CITTGYAYTQGLSGSILSLMGASAITGIMGTVAFTWLRKCGLVRTGLISGLAQLSCL 120
QY 386 LCVISVFMFGPGLDLSVSPFFEDIRSRFIOGESITP-TKIPE--ITTEIYMGNSNSANTV 442
Db 121 LCVISVFMFGPGLDLSVSPFFEDIRSRFVNVEPSPTKIPETVFTTEMENSNVN---V 176
QY 443 PETSPSPVPIISVSLFAGVIAARIGLMSFDTLVTQLQENVIESERGIINGVQNSMNYL 502
Db 177 HEMSTKPIPIVSVSLFAGVIAARIGLMSFDTLVTQLQENVIESERGIINGVQNSMNYL 236
QY 503 LDLLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFRQNTLGNKLFACGPDKEVRK 562
Db 237 LDLLHFIMVILAPNPAFGLLVLSVSVFVAMGHIMYFRQNTLGNKLFACGPDKEVRK 296
QY 563 ENQNTSVV 571
Db 297 ENQNTSVV 305

RESULT 13
Q7ZZ51 PRELIMINARY; PRT; 310 AA.
AC Q7ZZ51;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE SI:d246122.1 (Solute carrier family 39 (Iron-regulated transporter), member 1) (Fragment).
GN SLC39A1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

